72162

STIC-Biotech/ChemLib

From: STIC-ILL
Sent: Wednesday, July 31, 2002 6:32 AM
To: STIC-Biotech/ChemLib
Subject: FW: RE: 10/006,163

Imp rtance:

High

Request for you.

والمساف ومرام

-----Original Message-----

From: Huynh, Phuong N.

Sent: Tuesday, July 30, 2002 6:03 PM

To: STIC-ILL
Subject: RE: 10/006,163

Imp rtance: High

- 1. Please search polypeptide of SE SEQ NO: 1 (open) against commercial and interference database.
- 2. Also please do oligopeptide search of SEQ ID NO: 1 against commercial and interference database.

Thanks, Neon Art unit 1644 Mail 9E12 Tel 308-4844

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher:	
Phone:	
Location:	
Date Picked Up: 1/3/1/0/	
Date Completed 13/1/2	
Searcher Prep/Review:	
Clerical:	
Online time:	

TYPE OF S	EARCH:
NA Sequences: _	
AA Sequences: _	
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family: _	
Other:	

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
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Maximum Match 100%
Listing first 45 summaries
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                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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Copyright (c) 1993 - 2000 Com
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US-09-238-401-2
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Sequence

Query Match Best Local Similarity

100.0%;

Score 1623; DB 2; Pred. No. 2.8e-183;

Length 313;

INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 313 amino acids TYPE: amino acid STRANDENESS: single TOPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: PROSNOTO1 CLONE: 356351 US-09-019-216-1	APPLICATION NUMBER: FILING DATE: TORNEY/AGENT INFORMA NAME: Bilings, Luc RECETRATION NUMBER: REFERENCE/DOCKET NUM LECOMMUNICATION INFO TELEPHONE: 650-855- TELEFX: 650-845-41 TELEX:	ZIP: 94304 COMPUTER READABLE FORM: COMPUTER: IBM COMPATIBLE COMPUTER: FASTSED for Windows Version 2.0 CURRENT APPLICATION DATA: PRICE ADDITIONATION DATA: CLASSIFICATION DATA: CLASSIFICATION DATA:	L INFORMATICANT: LA ICANT: LA ICANT: CA ICANT: CA E OF INVEN ER OF SEQU ESPONDENCE ESPONDENCE DRESSEE: TREET: 317 TY: Palo TY: Palo TY: Palo	216-1 1, Appli	28 158.5 9.8 384 1 US-08-457-245-5 29 157.5 9.7 251 3 US-08-822-322-9 30 157.5 9.7 251 4 US-09-466-109-9 31 155.5 9.6 261 4 US-09-468-788A-29 32 155.5 9.6 333 1 US-08-40-856A-4 33 153 9.4 246 6 5229279-7 34 152.5 9.4 335 3 US-09-002-298-6 35 152.5 9.4 335 3 US-09-002-298-7 36 147 9.1 244 1 US-08-762-129-3 37 146 9.0 335 3 US-09-002-298-7 38 144.5 8.9 271 2 US-07-637-865-2 39 144.5 8.9 186 4 US-08-858-207A-270 40 141.5 8.7 309 3 US-09-109-205-1 41 137 8.4 244 1 US-08-762-129-4 42 136.5 8.4 244 1 US-08-762-129-4 43 136 8.4 255 4 US-08-815-225-4 44 135 8.3 244 1 US-08-762-129-1 45 132 8.1 292 4 US-09-468-738A-2
					Sequence 5, Appli Sequence 9, Appli Sequence 9, Appli Sequence 29, Appli Sequence 29, Appli Sequence 6, Appli Sequence 1, Appli Sequence 3, Appli Sequence 2, Appli Sequence 27, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

DB 2; 112;

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US-09-019-216-3
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                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEPHAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C
TITLE OF INVENTION: HUMAN SHORT CHAIN DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 51, CITY: Palo Alto
       LIBRARY: Genucians Conf. 2315796
                                                             TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSGLGWLASYLPSFLR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAACDKLAADCAHE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 VPKWIIALYTSKF 313
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                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/0:
FILING DATE: Filed Herewith
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                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                        ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALA 240
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                                                                                                                                      323 amino acids
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US-08-594-808B-7
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Best Local
                                       TELEX: 620420
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
SEQUENCE CASE amino acids
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tent No. 5804423
                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UNIFER.
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (718) 884-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sahm, Hermann
APPLICANT: Hollenberg, Cornelies P
TITLE OF INVENTION: MICROBIOLOGICAL METHOD
TITLE OF INVENTION: 5-KETOGLUCONATE
NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ARMSTDMAVELNPYNVCVVTLIPGPVKTETANRTIIDDAYKMIKENPELEE----FIKGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AQSLGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWE 110
                                                                                                                              TELEFAX:
                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/594,808B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM---AKEEVLQDPVLKQFKSAFSSAE
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                                                                                                                                718/601-1099
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N: 435
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Pred. No. 5e-64;
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US-08-594-808B-7

Matches Query Match

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Conservative

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Indels

Gaps

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256; 21;

Local Similarity

13.7%; 31.1%;

Score 222.5; DB 1 Pred. No. 8.9e-18; Mismatches

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65 SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL 124

5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64

LSGARALVTGASRGIGLTLAKGLARYGAEVVLNGRNAESLDSAQSGFEAEGLKASTAVFD 68

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MEDIUM TYPE: Floppy
                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                   FILING DATE: 20-JUL-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                        TELEPHONE: 713.787.1400
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NAVFFVGQAVARHMIPRGRGKIVNICSVQSELARPGI-----APYTATKGAVKNLTKGM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 RGHYFCSVYGARLMVPAGQGLIVVISS-----PGSLQYMFNVPYGVGKAACDKLAADC 177
                                                                                                                                                                                                                                                                                                                            FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 VTDQDAVIDGVAAIERD-MGPIDILINN--AGIQ-----RRAPLEEFSRKDWDDLMSTNV 120
                                                                                                                                                           NAME: Kammerer, Patricia A REGISTRATION NUMBER: 29,77
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
STRANDEDNESS:
                                                                                                                                            REFERENCE/DOCKET NUMBER:
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                               315 amino acids
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US-08-793-035-10
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Best Local
                                      NFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: GB95
APPLICATION NUMBER: GB95
APPLICATION TOWNS TOWNS TOWNS TO THE TOWNS TOWNS TO THE TOWNS TOWNS TO THE TOWNS T
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS
                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 NNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 VVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 HELRRHGVSCVSLWPGIVQTEL---LKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 IDLNLTGVFLCTQAATKIMMKKRKGRIINIASVVGLIGNIGQANYAAAKAGVIGFSKTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TFGGDVSKEADVEAMMKTA-IDAWGTIDVVVNN--AGI-----TRDTLLIRMKKSQWDEV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 AVPKVESPVVVVTGASRGIGKAIALSLGKAGCKVLVNYARSAKEAEEVSKQIEAYGGQAI 125
                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 PVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDI 119
                                                                                                                TELEPHONE:
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AAP-MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGASRNINVNVVCPGFIASDMTAKLGEDMEK----
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                                                                                  713.787
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Pred. No. 1.3e-
50; Mismatches
                                                                                                                                                                                                      MOBT: 132
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; STRANDEDNESS: s1; TOPOLOGY: linear US-08-793-035-10

Length 315;

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Best Local Similarity
Thes 72; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT ; ORGANISM: Staphylococcus aureus US-09-238-481-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/238,481
CURRENT FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09238481 Patent No. 6110704 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: FabG
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226 ASD 228
                                    240
                                                                      174 SRGITVNAVAPGFIVSDMTDALSDEL-KEQMLTQIPLARFGQD;DIANT---
                                                                                                        183 RHGVSCVSLWPGIV---QTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVAL 239
                                                                                                                                                                               130 CSVYGARLMVPAGQGLIVVISS------PGSLQYMFNVPYGVGKAACDKLAADCAHELR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 AVPKVESPVVVYTGASRGIGKAIALSLGKAGCKVLVNYARSAKEAEEVSKQIEAYGGQAI 125
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mes 75; Conserv
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                                                                                                                                                                                                                                                   70 EVRTLEEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGHYF 129
                                                                                                                                                                                                                                                                                                                            11 VVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCVPVVCDSSQES 69
                                                                                                                                                                                                                                                                                          8 LYTGASRGIGRSIALQLAEEGYNVAVNYAGSKEKAEAVVEEIKAKGVDSFAIQANVADAD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDLNLTGVFLCTQAATKIMMKKRKGRIINIASVVGLIGNIGQANYAAAKAGVIGFSKTAA 237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP-MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGASRNINVNVVCPGFIASDMTAKLGEDMEK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCA 178
                                                                                                                                             CTQKATPQMLRQRSGAIINLSSVVGAVGNPGQANYV-----ATKAGVIGLTKSAARELA
                                                                                                                                                                                                                   EVKAMIKEV-VSQFGSLDVLVNN--AGI-----TRDNLLMRMKEQEWDDVIDTNLKGVFN 119
                                    ATD 242
                                                                                                                                                                                                                                                                                                                                                                13.2%;
ilarity 29.6%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                               Score 214.5; DE Pred. No. 7.3e-1
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
3e-17;
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RESULT 8 US-09-466-109-8

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RESULT 7
US-08-822-322-8
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Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,322
FILING DATE: 21-March-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196
FILING DATE: 21-March-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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TELECOMMUNICATION INFORMATION:
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NAME: Hanson, No. 603711
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: ami
                                     230 ELSGKCV 236
                                                                                                                    171 DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSS-AETT 229
                                                                                                                                                                                               119 INNVGLRGHYFCSVYGARLMVPAGQGLIVV-----ISSPGSLQYMFNVPYGVGKAAC 170
222 DIAYICV
                                                                              168 KSAALDCA--LKDYDVRVNTVHPGYIKTPLVDDLPGAEEAMS----QRTKTPMGHIAEPN
                                                                                                                                                            110 LLAVNLDGVFFGTRLGIQRMKNKGLGASIINMSSIEGFVGDPSLGAY--NASKGAVRIMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                                                                                                                                           59 VPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                          58 QFFQHDSSDEDGWTKLFDATEK-AFGPVSTLVNNAGIAV-----NKSVEETTTAEWRK 109
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                                                                                                                                                                                                                                                                                                                                                 1 MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLG--GQC
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 28.7
71; Conservative
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228
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Alcohol dehydrogenase and its use for
enzymatic production of chiral hydroxy compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 196; DB 3; 28.7%; Pred. No. 1.2e-14;
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US-08-40-856A-3; Sequence 3, Application US/08440856A; Patent No. 5750873; GENERAL INFORMATION:
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Best Local
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hummel, Werner, Riebel, Bettina
TITLE OF INVENTION: Alcohol dehydrogenase and its use for
enzymatic production of chiral hydroxy compounds
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                                                                                                                                          222
                                                                                                                                                                                                                      168
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                                                                                                                                                                                                                                                                                                110 LLAVNLDGVFFGTRLGIQRMKNKGLGASIINMSSIEGFVGDPSLGAY--NASKGAVRIMS 167
                                                                                                                                                                                                                                                                                                                                        119
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NAME: HANSON, NO. 6225099man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLG--GQC 58
                                                                                                                                        DIAYICV
                                                                                                                                                                             ELSGKCV 236
                                                                                                                                                                                                                    KSAALDCA--LKDYDVRVNTVHPGYIKTPLVDDLPGAEEAMS----QRTKTPMGHIAEPN 221
                                                                                                                                                                                                                                                       DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSS-AETT 229
                                                                                                                                                                                                                                                                                                                                        INNVGLRGHYFCSVYGARLMVPAGQGLIVV-----ISSPGSLQYMFNVPYGVGKAAC 170
                                                                                                                                                                                                                                                                                                                                                                             QFFQHDSSDEDGWTKLFDATEK-AFGPVSTLVNNAGIAV-----NKSVEETTTAEWRK 109
                                                                                                                                                                                                                                                                                                                                                                                                                VPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSNRLDGKVAIITGGTLGIGLAIATKFVEEGAKVMITGRHSD---VGEKAAKSVGTPDQI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/466,109 FILING DATE: 17-Dec-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/822,322 FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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28.7%;
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Pred. No. 1.2e-14;
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Sequence 9, Application US/09413814 Patent No. 6225064

GENERAL INFORMATION:

APPLICANT: APPLICANT:

Bloecker, Helmut Brandt, Petra

Paul M

Beyer, Stefan Bristol-Myers Squibb,

APPLICANT: Gesellschaft fuer Biotechnologische Forschung APPLICANT: Bristol-Myers Squibb, Co.

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US-09-413-814-9
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Best Local
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                                                                 278 VEKMEEVVRGLATLKGPTLRPRDIAEAVLFLASDEARYISGHNLVVDGGVTTSRNLIGL 336
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ZIP: 20037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                      1 MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYI-----TGRHLDTLRVVAQEAQSL 54
                                                                                                                                                                                                                                                                                                                              MPKRLDGKVAIVTGGARGIGEAIVRLFAKHGARVVIADIDDAAGEAL-----ASAL 99
                                                                                                TELLKEHMAKEEVLQDPVLKQFKSA-----FSSAETTELSGKCVV----ALATDPNILSL 248
                                                                                                                                   TKNAACELRAHGVRVNCVSPFGVATPMLINAWRQGHDDATADADRDLDLDUDVTVPSDQE 277
                                                                                                                                                                                                   EFDRVLRVNALGAALGMKHAARAMAPRRAGSIVSVASVAAVLGGLGPHÄYTASKHAIVGL 217
                                                                                                                                                                                                                                MWDDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGS-LQYMFNVPYGVGKAACDKL 173
                                                                                                                                                                                                                                                                 GPQVSFVRCDVSVEDDVRRAVDWALSRHGGRLDVYCNN--AGVLGRQTRAARSILSFDAA 157
                                                                                                                                                                                                                                                                                                    GGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPAS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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VENTION: MATERIALS AND METHODS FOR PRODUCING

VENTION: PLANTS WITH SINGLE-SEX FLOWERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                     11.5%;
ilarity 27.4%;
Conservative 3
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SYSTEM: PC-DOS/MS-DOS
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linear
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APPLICANT: Dougherty, Brian A

PPLICANT:

Reichenbach, Hofle,

Hans

Mueller, Joachim

Gerhard

PPLICANT:

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                                                                                                                                                 NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 257
TYPE: PAT
ORGANIZM: Rhodobacter sphaeroides
US-09-287-097-2
                                 Query Match
Best Local Similarity
Matches 71; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09287097 Patent No. 6255093
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Best Local Similarity
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CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: DE/19815685.5 EARLIER FILING DATE: 1997-04-08
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                                                                                                                                                                                                                                                                                                                                               CURRENT
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: RECOMBINANT MICROBIAL 3-HYDROXYBUTYRATE DEHYDROGENASE, TITLE OF INVENTION: A PROCESS FOR ITS PRODUCTION AND THE USE THEREOF FILE REFERENCE: 1614-9007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or ITLE OF INVENTION: heteropolyketide compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SCHMUCK, Rainer
APPLICANT: MULLER, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ENGEL, Alfred
APPLICANT: KRUGER, Kerstin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: WEISSER, Harald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 AAYSIAKTGVLILTRSLATEEAPHGILVNCVS--PGLIDNGYLPPAQKEWMER 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 -PYGVGKAACDKLAADCAHELRRHG--VSCVSLWPGIVQTELL----KEHMAK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 LAAMTDDEWRNVMDSNLSSV----HYLCRAAVARMRQRKSGRIINIGLSPTYAIRGAPNV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 PASMWDD-----INNYGLRGHYFCSVYGARL-MVPAGQGLIVVISSPGSLQYMFNV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 RALGRRTMVVQADVTRPNAAAELESSVE-AQLGPIDILVNNV-------GDFFFKP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 QSLGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWET 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 AAPALPQARSLELAGRVALVTGSSRGIGKAIALRLAEQGADVAVNYHSNKDAAEQTAAEI 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AAP-----MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEA 51
5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYI---TGRHLDTLRVVAQE-AQSLGGQCVP 60
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/287,097 FILING DATE: 1999-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%;
                                                              11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 183.5;
; Pred. No. 5.2e
39; Mismatches
                                          36;
                                                                Score 178.5;
Pred. No. 1.
                                        Mismatches 105;
                                                                   : 4e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2e-13;
                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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                                          Indels
                                                                                       257;
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                                                                                                                                   Matches
                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                       TELEFAX: 630-252-2779
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40486
REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 AINLSSAFHTTAAALPGMRAKGWGRIVNIASAHGLTASPYKSAYVAAKHGVVGFTKVTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NVGLRGHYFCSVYGARLMVPAGQGLIV-VISSPGSLQYMFNVPYGVGKAACDKLAADCAH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IAADMSDGEACRALIETA-----GGCDILVNN--AGIQHV-----SSIEEFPVGKWNAIL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDIN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION:
                            65 SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL 124
                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: UPPER FILING DATE: 02/19/98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
 73
                                                                  13
                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ALWAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                            5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNGKRAIVTGSNSGIGLGCAEELARAGAEVVINSFTDRDED--HALAEKIGREHGVSCRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGQIGGTVV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELRRHGVSCVSLWPGIVQTEL-----LKEH-MAKEEVLQDPVL-----KQFKSAFSS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AETTELSGKCV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETAGKGITCNAICPGYVLTPLVEAQIPDQMKAHDMDRETVIREVMLDRQPSRQF-----
LTDMNAIDQLSQQI-MASVDHVDFLINNAGRSIRRAVHESFDRFHDFERTM-----
                                                                  VKGKVALITGASSGIGLTIAKRIAAAGAHVLLVARTQETLEEVKAAIEQQGGQASIFPCD
                                                                                                                                   69;
                                                                                                                                                    Similarity .
                                                                                                                                                                                                                                                                                         amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09026482B
                                                                                                                                                                                                                                                                                                       295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REISER, STEVEN E. SOMMERVILLE, CHRIS
                                                                                                                                                                                                                                                                                                                                                     630-252-27
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                 os: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC COMPATIBLE SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WORDPERFECT 6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEPARTMENT OF ENERGY GC-62 (FORSTL) MS-6F-067 OO INDEPENDENCE AVE. S.W.
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                                                                                                                                                                                                                                                                                    acid
                                                                                                                                                                                                                                                                                                      amino acids
                                                                                                                                                                                                                                   protein
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                                                                                                                                                   10.9%;
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                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                         S-87814
                                                                                                                                 Score 176.5; DB 4;
Pred; No. 3.1e-12;
B; Mismatches 115;
                                                                                                                                     Indels
                                                                                                                                                                  Length 295;
                                                                                                                                     51;
                                                                                                                                   Gaps
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                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 838-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: PASQUALINI, PATTICIA A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 6-Octob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 QLNYFGAV---RLVLNLLPHMIKRKNGQIINISSIGVLANATRFSAYVASKAALDAFSRC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 LSAEVLKHKISITSIYMPLVRTPM------IAPTKIYKYVPTLSPEEAADLIVYAI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/375,962B FILING DATE: 20-January-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLE OF INVENTION:
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                   G
                                                                                                                                                                                                                                                                                                                      ENGTH:
                                              GQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCDSS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKRPTRIATHLGRLASITYAIAPDINNILMSIGFNLFPSSTAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York City
                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHRISTER; ERIKSSON, ULF.

IVENTION: Isolated Nucleic Acid

VENTION: Which Codes for A 32 h
                                                                                                                                                                                                                                                                                                                 244 amino acids
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
                                                                                                                                                                                                        E.coli 3-oxoacyl[acyl carrier protein]
reductase (FABG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HBM
                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette, 3.5 inch, 144 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6-October-1994
                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                   838-3884
                                                                                                                             10.5%;
                                                                                                                                                                                                                                                                                                                                                                                    688-9200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ALATDPN--ILSLSGKVLPSCDLA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08/258,418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   solated Nucleic Acid Molecule
hich Codes for A 32 kDa Protein Having 11-CIS Retinol
ehydrogenase Activity, and Which Associates With P63,
Portion of a Retinol Binding Protein Receptor
                                                                                                              45;
                                                                                                                             Score 171;
Pred. No. 1
                                                                                                              Mismatches 111;
                                                                                                                            1e-11;
                                                                                                                                          DB 1; Length 244;
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                                                                                                              Indels 30;
                                                                                                           Gaps
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                                                                                                                                                                                         ; NAME/KEY:
US-08-562-114B-13
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Patent No.
                                                                                                              Matches
                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ERIKSSON TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPEFFECT 5.1 and ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 20-January-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 ITVNVVAPGFIETDMTRALSDDQRAGILAQVPAGRLGGAQEIANAVAFLASDEAAYITGE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 VFRLSKAVMRAMMKKRHGRITTIGSVVGTMGNGGQANYAAAKAGLIGFSKSLAREVASRG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 TLHVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 TTELSG 233
                                                                                                                                                                                                                                                                                        TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 22-No. CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
NAME: Kohli, Vineet REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                       NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
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                                             GKIALVTGASRGIGRAIAETLAARGGKVIGTATSENGAQAI----SDYLGANGKGLMLNVT 61
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1: 805 Third Avenue
New York City
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24.4%;
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                                                                                                                           Score 171;
Pred. No. :
                                                                                                            Mismatches
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     Best Loc
Matches
                   Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
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                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,946
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SOFTWARE: Wordper
                                                                                                                NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
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TLING DATE: 22-No.
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I: 805 Third Avenue
New York City
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                 10.5%; Score 171; DB 4 24.4%; Pred. No. 1e-11;
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   Mismatches
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Search completed: July 31, 2002, 15:09:36 Job time: 125 sec

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Title:
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000 Compugen L
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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•	fixR homolog - Agr	probable carbonyl	3-oxoacyl-[acyl-ca	short chain dehydr	probable short-cha	<pre>probable short-cha</pre>	3-oxoacyl-(acyl-ca	gluconate 5-dehydr	ribitol-5-phosphat	NAD/NADP dependent	3-oxoacyl-(acyl-ca	probable 3-oxoacyl	3-oxoacyl-(acyl-ca	3-oxoacyl-[acyl-ca	3-oxoacyl-[ACP] re	3-oxoacyl-[acyl-ca

ALIGNMENTS

Query Match 5.1%; Score 16; DB 2; Length 32 Best Local Similarity 100.0%; Pred. No. 1.7e-08; Matches 16; Conservative 0; Mismatches 0; Indels Qy 12 VTGASRGIGRGIALQL 27	C:Species: Caenorhabditis elegans C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C:Accession: 732125 R;Bradshaw, H. submitted to the EMBL Data Library, July 1997 A;Description: The sequence of C. elegans cosmid F59E11. A;Reference number: 221124 A;Accession: 732125 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-323 <bra> A;Cross-references: EMBL:AF016685; PIDN:AAB66216.1; GSPDB:GN00023; CESP:F59E11.2 A;Experimental source: strain Bristol N2; clone F59E11 C;Genetics: A;Gene: CESP:F59E11.2 A;Map position: 5 A;Introns: 20/1; 60/1; 108/3; 135/2; 166/2; 192/3; 227/3; 280/1</bra>	RESULT 1 T32125 hypothetical protein F59E11.2 - Caenorhabditis elegans
DB 2; Length 323; 1.7e-08; nes 0; Indels 0; Gaps	1999 #text_change 29-Oct-19 1d F59E11. /DDBJ 16.1; GSPDB:GN00023; CESP:E e F59E11	elegans
0,	99 59E11.2	

SULT 2

AH2042
3-oxoacyl-[acyl-carrier protein] reductase [imported] - Anabaena sp. (strain PCC 71: C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AH2042

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iri(Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabai DNA, Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A; Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2042
A;Status: preliminary A;Accession: AH2042
A;Cross references: GB:BA000019; PIDN:BAB73593.1; PID:g17130984; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

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J. Biol. Chem. 267, 5751-5754, 1992
A;Title: The gene encoding Escherichia coli
A;Reference number: A42147; MUID:92210530
A;Molecule ***
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A; Molecule type: DNA
A; Residues: 1-42, 'R', 44-45 <VER>
A; Residues: 1-42, 'R', 44-45 <VER>
A; Cross-references: GB: M87040; NID: g145885; PIDN: AAA23743.1; PID: g145888
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence inconsistent with the nucleotide translation with the nucleotide t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Pathway: fatty acid biosynthesis
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
C;Keywords: fatty acid biosynthesis; NADP; oxidoreductase
F;6-182/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;6-36/Region: beta-alpha-beta NADP nucleotide-binding fold
F;151/Active site: Tyr #status predicted
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A; Residues: 1-29, (G', 31-244 < RAN>
A; Residues: 1-29, (G', 31-244 < RAN>
A; Residues: 1-29, (G', 31-244 < RAN>
A; Cross references: GB. M84991; NID: 9145879; PIDN: AAA23739.1; PID: 9145881
A; Verwoert, I.I.; Verbree, E.C.; van der Linden, K.H.; Nijkamp, H.J.; St.
J. Bacteriol. 174, 2851-2857, 1992
A; Title: Cloning, nucleotide sequence, and expression of the Escherichia A; Reference number: A41856; MUID: 92234941
A; Accession: C41856
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RESULT 4

939812

3-oxoacyl-[acyl-carrier-protein] reductase [imported] -
C;Species: Escherichia coli
C;Date: 18-Jul-2001 *sequence_revision 18-Jul-2001 *text
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C;Species: Escherichia coli
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B42147
3-oxoacyl-{acyl-carrier-protein] reductase (EC 1.1.1.100)
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A; Residues: 1-244 <BI
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C; Function:
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                                                                                                                                3-oxoacy1-{acy1-carrier-protein} reductase (EC 1.1.1.100) [imported] - Moritella C; Species: Moritella marina C; Species: Moritella marina C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000 C; Accession: T44434 R; Morita, N.; Ueno, A.; Tanaka, M.; Ohglya, S.; Hoshino, T.; Kawasaki, K.; Yumoto Biotechnol. Lett. 21, 641-646, 1999 A; Title: Cloning and sequencing of clustered genes involved in fatty acid biosynt
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   A; Reference number: Z22768
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A; Status: preliminary; tran
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K.Hayası.., N.; Yasunaga, T.; Kuhara, .... gasawara, N.; Yasunaga, T.; Kuhara, .... Egasawara, N.; Yasunaga, T.; Kuhara, .... Egasawara, N.; Yasunaga, T.; Kuhara, .... Each R.; Yasunaga, Each R.; Yasunaga, T.; Kuhara, .... Each R.; Yasunaga, T.; Kuhara, .... Each R.; Yasunaga, E
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A; Molecule type: DNA
A; Residues: 1-244 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB34894.1;
A; Cross-references: Strain O157:H7, substrain F
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                                                                                                                                                                                                                                                       C;Function:
Atty acid biosynthesis
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
C;Keywords: fatty acid biosynthesis; NADP; oxidoreductase
F;6-182/Domain: short-chain alcohol dehydrogenase homology <SAD>
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C;Date: 16-Jul-1999 #sequence_revision
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C; Superfamily: ribitol dehydrogenase;
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A; Title: Isolation of Vibrio
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Yasunaga, T.; Kuhara,
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source: strain B392
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Shiba, T.; Hattori, I
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A;Residues: 1-244 <MOR>
A;Cross-references: EMBL:AB021978; PIDN:BAA85256.1
A;Experimental source: ATCC 15381
C;Genetics:
                                                                                                                                                                   A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AB0195
                                                                                                                                                                                                                                    R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, II. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barro, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                          3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) [imported] - Yersinia C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001 C;Accession: AB0195
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AB0195
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C;Keywords: oxidoreductase
                                                                                                        A; Molecule type: DNA
A; Residues: 1-244 < KUR>
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Nature 409, 529-533, 2001
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                                                                      A;Cross-references: GB:AL590842; PIDN:CAC90421.1; PID:g15979637; GSPDB:GN00175
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Best Local Similarity
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Best Local Similarity
Matches 10; Conserv
Superfamily: ribitol dehydrogenase; short-chain Keywords: oxidoreductase
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                  alcohol dehydrogenase homology
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Barrell,
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C;Accession: AD0642
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churc th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far
                                                                                                                                                                                                                                                                                                                                    C;Accession: B83462
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-oxoacyl-[acyl-carrier protein] reductase [imported] - Salmonel C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AD0642
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C; Superfamily:
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C; Superfamily:
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A; Residues: 1-244 <PAR>
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                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-245 <STO>
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                                                Matches
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             21
                                                                                                                                                                                                                                                                                                    sequence of Pseudomonas aeruginosa PAO1, 50; MUID:20437337
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0.029;
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A.; Larbig,
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A;Experimental source: Strain 168
C;Genetics:
A;Gene flab; srb
A;Map position: 135-145 degrees
C;Function:
C;Function: EC 1.1.1.100 [validated, MUID:96326321],
A;Pathway: fatty acid biosynthesis
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: fatty acid biosynthesis; NADP; oxidoreductase
F;5-185/Domain: short-chain alcohol dehydrogenase homology
F;154/Active site: Tyr #status predicted
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A,Molecule type: DNA
A;Residues: 1-22,'A',24-246 <CRO>
A;Cross-references: EMBL:U59433; NID:g1502418; PIDN:AAC44307.1; PID:g1502421
                     RESULT 12

C83961
3-oxoacyl-(acyl-carrier protein) reductase fabG [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
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A;Residues: 230-246 \( \text{OGU} \)
A;Residues: 230-246 \( \text{OGU} \)
A;Cross-references: DDBJ:D64116; NID:g1389548; PIDN:BAA10974.1; PID:g1237012
R;Cronan, J.E.; Morbidoni, H.R.; de Mendoza, D.
J. Bacteriol. 178, 4794-4800, 1996
A;Title: Bacillus subtilis acyl carrier protein is encoded in a cluster of lipid biosynt A;Reference number: 223107; MUID:96326321
A;Accession: 746633
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A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Accession: A69821
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R;KunSt, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Mature 390, 249-256, 1997
A:Authbors. Politics D. Fritt C. Fritte M. D. Fritze M. D. Fritte M.
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N;Alternate names: 3-ketoacyl-acyl carrier protein reductase
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9 VTGASRGIGR 18
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#sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
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                                                                                                                              A;Reference number: A82950; MUID:20437337

A;Recession: G83253
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83253
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hic) adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lari; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A; Status: preliminary

probable short-chain dehydrogenase PA3128 [imported] - Pseudomonas aeruginosa (strain

Hickey, Larbig,

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3-OXOacyl-(acyl-carrier protein) reductase [imported] - Staphylococcus aureus (straic) species: Staphylococcus aureus (c) species: Staphylococcus aureus (c) species: O-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 (c) Accession: B89896 (c) T.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Cui, L.; R; Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A.; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                     A:Status: preliminary
A;Molecule type: DNA
A;Residues: 1-246 <KUR>
A;Cross-references: GB:BA000018; PID:g13701031; PIDN:BAB42326.1;
A;Experimental source: strain N315
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C; Superfamily: ribitol dehydrogenase;
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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R;Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83961
A;Status: preliminary
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-246 <STO>
A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06210.1; GSPDB:G
A;Experimental source: strain C-125
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Pred. No.
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A;Note: gra-orf6
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: NAD; oxidoreductase
F;9-187/Domain: short-chain alcohol dehydrogenase homology <SADH>
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Title: Structure and deduced function of the granaticin-producing polyketide synthase;Reference number: S05393; MUID:90060034
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MBO J. 8, 2717-2725, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Streptomyces violaceoruber
;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 11-May-2000
;Accession: S05398; T46535
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:Ichinose, K.; Bedford, D.J.; Tornus, D.; Bechthold, A.; Bibb, M.J.; Revill, W.P.; Flosem. Biol. 5, 647-659, 1998
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'A. Conservative 0; Mismatches
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sp_phage:*
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Q913p2 pseudomonas
Q96a03 bacillus ha
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Q9fbx4 streptomyce	Q9k3y8 streptomyce	Q9jw61 neisseria m	Q9jxr1 neisseria m				Q9uy54 pyrococcus	Q49154 methylobact				Q93x62 brassica na		Q949m3 brassica na	Q9s0n7 streptomyce		IΛ	_		drosophi		Q987c7 rhizobium 1	. Q9alp1 saccharopol	Q9rt26 deinococcus	N	Ų,		Q92rll rhizobium m

ALIGNMENTS

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96LJ7; PRELIMINARY; PRT; 313 AA. 96LJ7; PRELIMINARY; PRT; J. Last sequence update) 1-DEC-2001 (TrEMBLrel. 19, Last sequence update) 1-DEC-2001 (TremBle 19, Last sequence upda	QΥ	g 4g) B	Оу	Ma Do	S	DR	RL	RT	R.A	RA A	₽ P	R.	RA	R C	RP	RN	0×	റ്റ	g	S	DΕ	ij	뎟	ņ	AC	Đ S	RESU	
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Query Match
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Q96CQ5;
Q1-DEC-2001 (TIEMBLrel. 19, Created)
O1-DEC-2001 (TIEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TIEMBLREL. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 1110029G07 GENE.
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Homo sapiens (Human).
Homorota; Metazoa; Chordata;
heria; Primates;
                                                                                                        Strausberg R.;
Strausberg R.;
SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC014057; AAH14057.1;
SEQUENCE 313 AA; 33925 MW; 37FA022675C4F076 CRC64;
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Q96B59;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HTPDTHETICAL 33.9 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-PANCREATIC ADENOCARCINOMA;
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Submitted (OCT-2001) to the
EMBL; BC015943; AAH15943.1;
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SEQUENCE 313 AA; 33881 MW;
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TISSUE-MELANOMA;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Riyosawa H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashiraki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 39
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                                                                                                                                                                                                                                                   Hayashizaki Y.;
"Functional annotation of a full-
Nature 409:685-690(2001).
EMBL; AK003958; BAB23093.1;
MGD; MGI:1915960; 1110029G07Rik.
SEQUENCE 313 AA; 34031 MW; 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           History (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9D148;
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                                                                                                             SHVSGLGWLASYLPSELRVPKWIIALYTSKF 313
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                                                                                                                                                                                           Similarity
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17,
17,
19,
                                                                                                                                                                        0;
                                                                                                                                                                      Score 39; DB Pred. No. 5.600; Mismatches
                                                                                                                                                                                                                                                                                                           full-length
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Last
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                                                                                                                                                                                         DB 11;
5.6e-3;
                                                                                                                                                                                                                                                                                                           mouse
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thes 0;
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on update)
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; Murinae; Mus
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Best Local S
Matches 39
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Q9N538;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Nematoda; Chromadorea;
      (SDR) FAMILY.

EMBL: ACCO6733; AAF60486.1; -.

HSSP; P50162; 1AE1.

InterPro; IPR002198; ADH_short.

PRINTS; PR00080; SDRFAMILY.

PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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                                                              *Direct Submission.";
Submitted (JUL-2001) to
-1- SIMILARITY: BELONGS
                                                                                                                              STRAIN-BRISTOL N2;
Holmes A., Elliot G., Cloud
"The sequence of C. elegans
Submitted (MAR-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Hypothetical
                                                                                                    STRAIN-BRISTOL N2;
                                                                                                                                                                                     "Genome sequence of the nematode investigating biology. The C. ele science 282:2012-2018(1998).
                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                            Waterston
                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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1 (TrEMBLrel. 19; Las
AL 35.1 KDA PROTEIN.
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protein;
                                                                                                                                                                                                                                       N2;
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                                                                                                                                                                                                                              PubMed=9851916;
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Rodentia;
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Oxidoreductase
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                                                               EMBL/GenBank/DDBJ databases.
THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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Last sequ
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cosmid Y32Hl2A.";
EMBL/GenBank/DDBJ
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HE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39;
Pred. No.
                                                                                                                                                                                               ode C. elegans: a platform elegans Sequencing Consort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPHA MODEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
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5.6e-31;
hes 0;
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                                                                                                                                databases
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                                                                                                                                                                                                 Consortium.";
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; Murinae; Mus
                                                                                                                                                                                                                                                                                     Rhabditoidea;
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016764;
01-JAN-1998 (TrEMBLrel. 05, Created)
T 01-JEC-2001 (TrEMBLrel. 19, Last segon 1-DEC-2001 (TrEMBLrel. 19, Last an ""POTHETICAL 35.8 KDA PROTEIN."
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Best Local S
Matches 16
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Best Local
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Q9K486
Q1-Q7-2000 (Tremblrel. 1
01-Q7-2000 (Tremblrel. 1
01-Q7-2000 (Tremblrel. 1
01-DC7-2001 (Tremblrel. 1
PUTATIVE OXIDOREDUCTASE.
SC7E4.34C.
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002198; ADH_short.

Pfam; PF00106; adh_short; 1.

Hypothetical protein; Oxidoreductase.

SEQUENCE 323 AA; 35824 MW; 4FE24D30ED39CAE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Direct Submission.";
Submitted (AUG-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradshaw H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF016685; AAG24139.1;
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                                                                                                                                                                                                                                                                                                                                                  ch 5.1%;
1 Similarity 100.0%;
16; Conservative
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l Similarity 100.0%;
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . elegans
7) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematoda; Chromadorea; cinae; Caenorhabditis.
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THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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EMBL/GenBank/DDBJ
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Pred. No. 1.3
0; Mismatches
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                                                                                         Wang L., Vining L.C.;
"Control of antibiotic biosynthesis and cell differentiation in Streptomyces venezuelae ISP5230 by JadW1, a homolog of the gamma butyrolactone autoregulators Barx and Afsa.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 024659; AAL23836.1;
EMBL; 024659; AAL23836.1;
SEQUENCE 254 AA; 26434 MW; 4347A4FEE372B752 CRC64;
                                                                                                                                                                                                             Streptomyces venezuelae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                               Q934T1 PRELIMINARY;
Q934T1;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                      01-DEC-2001
                                                                                                                                                                              STRAIN-ISP5230;
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SEQUENCE 250 AA;
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HSSP; Q12634; 1YBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the 8 Mb Streptomyces coelicolor A3(2)
Mol. Microbiol. 21:77-96(1996).
-I- SIMILARITY: BELONGS TO THE SHORT-CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeger K.J., Harris |
Submitted (JUN-2000)
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Kinashi H., Hopwood D.A.;
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
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                                           Conservative
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                                      4.2%; 500
100.0%; Pr
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e EMBL/GenBank/DDBJ databases.
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Best Local :
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Morita N., Ueno A., Tanaka M., Ohgiya S., F
Yumoto I., Ishizaki K., Okuyama H.;
"Cloning and sequencing of clustered genes
biosynthesis from the docosahexaenoic acid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q47202;
Q47202;
Q1-NOV-1996
                                                                                                                                                                                            Biotechnol. Lett. 21:641
      Oxidoreductase SEQUENCE 244
                                          PRINTS; PRO0080; SDRFAMILY, PROSITE; PS00061; ADH_SHORT
                                                                                      InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
                                                                                                                                EMBL; AB021978; BAA85256.1; -. HSSP; P19992; 1HDC.
                                                                                                                                                                                                                                         marinus strain MP-1."
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01-DEC-2001
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01-MAY-2000 (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio marinus (Moritella
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Stuitje A.R.;
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EMBL; M87040; AAA23743.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                             CBI_TaxID=90736;
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25558 MW; 871DD5CF7B7F00E3 CRC64;
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SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

STOVER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrene Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lac Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yugarber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yugarber R.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lim Brody L.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
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01-MAR-2001
01-DEC-2001
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01-NOV-1998
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086853;
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"Characterisation of scbr, and scbr genes involved in gamma-
butyrolactone binding and synthesis in Streptomyces coelicolor.";
submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTA.
                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE SHORT-CHAIN DEHYDROGENASE.
                                                                                                                                                                       Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                         Q9I3P2
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Pfam; PF00106; adh_short; 1.
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PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
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                                                                                                                                                 NCBI_TaxID=287;
                                                                                                                                                               Pseudomonas
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Q12634; 1YBV
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Q984V1;
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Q9KA03;
01-OCT-2000
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EMBL; AE004576; AAG04859.1;
HSSP; Q12634; 1YBV.
                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Oxidoreductase.
SEQUENCE 246 AA; 26126 MW; 852B95EB8DEE9E90 CRC64;
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MEDLINE-20512582; PubMed-11058132;
Takani H., Nakasone K., Takaki Y., Maeno G., S.
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
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SEQUENCE 245 AA; 25365 MW; 342AlCF12C500744 CRC64;
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Pfam; PF00106; adh_short; 1.
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Nature 406:959-964(2000).
-!- SIMILARITY: BELONGS T
    PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        halodurans and genomic sequence comparison Nucleic Acids Res. 28:4317-4331(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome sequence of the alkaliphilic bacterium alodurans and genomic sequence comparison with Bacillu.
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; PS00061; ADH_SHORT; UNKNOWN_1.
2001 (TrEMBLrel. 1
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E OXIDOREDUCTASE.
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                                                                                                              PRELIMINARY;
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                  18,
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PROTEIN) REDUCTASE (EC 1.1.1.100).
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Page 6
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OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TAXID=381;
RN [1]
RN [2]
RN STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
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RA Watnabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
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RA Kaneko T., Nakamura Y., Sato S., Natsuno A.,
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RA Watnabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:13:57; Search time 13.51 Seconds (without alignments) 897.055 Million cell updates/sec

Title: Perfect score: Sequence: US-10-006-163-1 313

1 MAAPMNGQVCVVTGASRGIG.....YLPSFLRVPKWIIALYTSKF 313

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : Post-processing: Listing first 45 summaries SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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VST2_HEVRH	RCA_LYCPN	PYRC_BACCL	CYSL_SPIOL	TALA_ECOLI	LPPW_MYCTU	E434_ADE02	E434_ADE09	PTR1_LEITA	PTR1_LEIMA	DHKR_STRCM	ACT3_STRCO
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ALIGNMENTS

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DE	Aflatoxin biosynthesis	
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88	Aspergillus parasiticus.	
88	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomy	
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2 5	STRAIN-ATCC 163 /	
RX :	MEDLINE-95085270;	
RA	Trail F., Chang PK., Cary J., Linz J.E.;	
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1 7	prosynthesis of affacoxins by Aspergittus parasitions	
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S	-I- PATHWAY: AF	
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38	(SDR) PRIMER STRONG, TO ENTROPHING STCE.	
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36	use by non-profit institutions as long as its content is in no	2 % a y
8	entities requires a license agreement (See http://www.isb-sib.c)	ice/
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o O	Match 3.5%; Score 11; DB 1;	
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EMBL; AE000210; AAC74177.1; -.
EMBL; D90745; BAA35901.1; -.
EMBL; B42147; B42147.
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-I- CAPALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]

-I- MADP(+) - 3-oxoacyl-[acyl-carrier protein] + NADPH.

-I- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSNIMA T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                     EcoGene; EG11318; fabG.
EcoGene; EG11318; fabG.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; Adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-fabg OR B1093.
                                                           CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97061202;
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STRAIN-K12 / 1
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J. Biol. Chem. 267:5751-5754(1992).
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; PS00061; ADH_SHOR
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SPECIES-S. typhi; STRAIN-CT18;

MEDLINE-21534947; PubMed-11677608;

MARCHINE-21534947; PubMed-11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.

Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

Feltwell T., Hamlin N., Haque A., Hlen T.T., Holroyd S., Jagels K.,

Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitchead S., Barrell B.G.;

Whitchead S., Barrell B.G.;
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30-MAY-2000
30-MAY-2000
                                                                                               -!- SIMILARITY: BELONGS
                                                                                                                      -i- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
-i- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                           "Complete genome sequence of a multiple enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McClelland M., Sanderson K.E., Spieth J., Clifton S.W., La Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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MEDLINE-98317265; PubMed-9642179;
Zhang Y., Cronan J.E. Jr.;
"Transcriptional analysis of essential genes of the Escherichia fatty acid biosynthesis gene cluster by functional replacement withe analogous Salmonelia typhimurium gene cluster.";
Ch. Bacteriol. 180:3295-3303(1998).
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (E
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Salmonella typhi.
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FABG OR STM1195 OR STY1234.
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                                                                                         SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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*Isolation of Vibrio harveyi acyl carrier protein; ";
and fabf genes involved in fatty acid biosynthesis; ";
J. Bacteriol. 178:571-573(1996).
-I- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]
NADP(+) = 3-oxoacyl-[acyl-carrier protein] +.NADPH.
-I- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
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01-OCT-1996 (Rel.
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Bacteria; Proteobacteria;
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                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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NADP(+) = 3-oxoacyl-[acy
- I - PATHWAY: FIRST REDUCTION
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Submitted (NOV-1997)
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                                                                                                                                                                                                                       Oguro A., Kakeshita I
Submitted (MAR-1996)
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"Bacillus subtilis acyl carrier pr
ilpid biosynthesis genes.";
J. Bacteriol. 178:4794-4800(1996).
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to the EMBL/GenBank/DDBJ databases
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Best Local
                                                                                                                                           Antibiotic biosynthesis; Oxidoreductase; NAD.
NP_BIND 12 36 NAD (BY SIMILARITY).
ACT_SITE 157 157 BY SIMILARITY
SEQUENCE 249 AA; 25977 MW; 922832B88FE34A8B CRC64;
                                                                                                                                                                                                                                                                                                                                   EMBL; X16300; CAA34367.1;
EMBL; X16144; CAA34262.1;
PIR; S05398; S05398.
                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHK2_STRVN
P16543;
01-AUG-1990
                                                                                                                                                                                                                                     Pfam: PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Granaticin polyketide synthase putative ketoacyl reductase
(EC 1.3.1.-) (ORF6).
Streptomyces violaceoruber.
Hactoria.
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CONFLICT
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Sherman D.H., Malpartida F., Bibb M.J., Kieser H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
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                                        Local Similarity 100 hes 10; Conservative
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84 GRLDVLVNNA
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9 VTGASRGIGR 18
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PATHWAY: BIOSYNTHESIS OF THE POLYKETIDE ANTIBIOTIC GRANATICIN.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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9 33 NADP (BY SIMILARITY).
154 154 BY SIMILARITY.
23 D -> A (IN REF. 1).
246 AA; 26282 MW; C6A391167D3237DC CRC64;
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FABG OR VC202
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01-OCT-1996
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                                                                                               CBI_TaxID-666
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271 AA;
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(Rel. 40, Last sequence up
(Rel. 40, Last annotation
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RESULT 9
FABG_PSEAE
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

X MEDLINE-99395062; PubMed-10464226;

X MEDLINE-99395062; PubMed-10464226;

X Kutchma A.J., Hoang T.T., Schweizer H.P.;

A Kutchma A.J., Hoang T.T., Schweizer H.P.;

Characterization of a Pseudomonas aeruginosa fatty aci

"Characterization of acyl carrier protein (ACI

"Tore coenzyme A:ACP transacylase (fabb).";

"Toreriol. 181:5498-5504(1999)."
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Best Local S
Matches 9
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O54438;
O55452;
O55652;
O56552;
O57552;
O57552
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FABG OR PA2967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FABG_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004276; AAF95169.1; ALT_INIT.
TIGR; VC2021; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
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1 - CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]

NADP(+) = 3-cxoacyl-[acyl-carrier protein] + NADPH.

1 - PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholerae
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Heidelberg J.F., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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PF00678; adh_short_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid biosynthesis; Oxidoreductase; NADP; Complete

ND 10 34 NADP (BY SIMILARITY).

ITE 151 151 BY SIMILARITY.

NCE 244 AA; 25566 MW; 9FB2E8278D7CC3CE CRC64;
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10952301;
Eisen J.A., Nelso
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision; Pseudomonadaceae;
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. 0.15;
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                                                                                                                                                                                                                 osa fatty acid
protein (ACP)
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SOLUTION DE LA PRESENTATION DE L
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FRAGI_SYNY3 STANDARD; PRT; 247 AA.

ID FAGI_SYNY3 STANDARD; PRT; 247 AA.

AC P73574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-cxoacyl-[acyl-carrier protein] reductase 1

DE 3-cxoacyl-[acyl-carrier protein] reductase 1
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Best Local
Matches
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MEDLINB-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.

Brody L.L., Coulter S.N., Folger K.R., Kest A., Larbig K., Lim R.M.

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
Fatty aci
NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hosouchi
Shimpo S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statishent is not removed. Usage by and for commodified and this statishent is not removed. Usage by and for commodified and this statishent is not removed.
"Sequence analysis of the genome of the Synechocystis sp. strain PCC6803. II. Seentire genome and assignment of potentia DNA Res. 3:109-136(1996).
                                                                                               Shimpo S.,
Tabata S.;
                                                                                                                                                                                                                                                                                          Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U91631; AAB94395.1; -.
EMBL; AE004722; AAG06355.1; -.
HSSP; 012634; 1YBV.
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                                                                                                                                                                                            MEDLINE-97061201; PubMed-8905231; Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                                                                                                                                                                                                       ketoacyl-acyl carr
FABG1 OR SLR0886.
                                                                                                                                                                          Miyajima
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SIMILARITY: BELONGS
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; PR00080; SDRFAMILY.
E; PS00061; ADH_SHORT; 1.
E; PS00061; ADH_SHORT; 1.
Oxidoreductase; NADP; Complete
D 10 34 NADP (BY SIMILARITY).
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9; Conser
                                                                                                                    ., Sato S., Kotani H., Tanaka A., Asamizu E.,
N., Hirosawa M., Sugiura M., Sasamoto S., Kin
T., Matsuno A., Muraki A., Nakazaki N., Naruu
T., Takeuchi C., Wada T., Watanabe A., Yamada N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002198; ADH_short
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247 AA;
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Pred. No.
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    II. Sequence determination potential protein-coding regi

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. 0.15;
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                                                                        unicellular cyanobacterium
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                                                                                                                       S., Kimura T.,
, Naruo K., Okumu
mada M., Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                           1.1.1.100)
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                                                                                                                                                   Okumura
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RESULT 11
GNO_GLUOX
ID GNO_G
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Best Local :
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNO_GLUOX
P50199;
01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                              NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-DSM 3503;
MEDLINE-95270578; PubMed-7751271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Last 16-OCT-2001 (Rel. 40, Last Gluconate 5-dehydrogenase /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., SEQUENCE OF 3-19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gluconobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gluconobacter oxydans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fatty acid blosynthesis; Oxidoreductase; NADP; Complete proteome.

NP_BIND 11 35 NADP (BY SIMILARITY).

ACT_SITE 156 156 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00106;
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                                                                                                                                                                                                       SUBCELLULAR LOCATION:
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NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.

PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS

PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 2.9%; So Similarity 100.0%; ; 9; Conservative 0;
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0106; adh_short; 1.
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247 AA;
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                                                                                                                                                                              BELONGS
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ria; alpha subdivision; Ace
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Last annotation update)
hase (EC 1.1.1.69) (5-keto-D-gluconate
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                                                                                                                                                       Cytoplasmic.
O THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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Best Local
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01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001-(Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                 EMBL; X64566; CAA45866.1;
PIR; S19832; S19832.
                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         use by non-profit institumodified and this statement
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-!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]

NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.

-!- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eleurosids II; Myrtales; Lythraceae; Cuphea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY:
-!- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Isolation and characterization of a cDNA encoding a beta-ketoacyl-ACP reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein B., Pawlowski K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92293104;
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ACT_SITE
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9; Conserv
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27256 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoericke-Grandpierre C.,
                                                                                                                                                                                                            is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
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0; Mismatches
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BY SIMILARITY.
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.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eudicots;
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PRINTS; PR00080; SDRFAMILY. PROSITE; PS00061; ADH_SHORT InterPro; IPR002198; ADPriam; PF00106; adh_shor

biosynthesis;

Oxidoreductase;

NADP; Chloroplast;

HSSP; P50162; 1AE1.

IPR002198; ADH_short.

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RESULT 13
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PIR; S48498; S4849b.
SGD; S0001475; YIR038C.
SGD; S0001475; YIR038C.
A InterPro; IPR002198; ADH_short.
A Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; 1.
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Churcher C.M., Connor R., Copsey T., Dear S., Devlin
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels
Louis E., Lye G., Moule S., Moule T., Odell C., Pears
Rajandream M.A., Riles L., Rowley N., Skelton J., Smi
Walsh S.V., Whitehead S., Rowley N., Skelton J., Smi
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RESULT 14
DHCA_HUMAN
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A Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
A Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
A Rosenthal A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E
A Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E
A Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
A Lehrach H., Reinhardt R., Yaspo M.-L.;
The DNA sequence of human chromosome 21.";
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P16152;
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01-APR-1993 (Rel.
16-OCT-2001 (Rel.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Homo sapiens (Human)
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MEDLINE-20289799; PubMed-10830953;
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                                                                                                 Nitrogen fixation; Oxidoreductase.
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Pfam; PF00106; adh_short; 1.
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Human endocrine po	834	22	357		197	5
Arabidopsis thalia	$\bar{\omega}$	21	307		197.5	44
is thai	AAG40333	21	285		197.5	43
thal	3550	21	308		199.5	42
is thal	AAG12861	21	307	12.3	199.5	41
••	286	21	285		199.5	40
thal	550	21	267		199.5	39
sequ	436	22	418		202.5	38
AFP	126	22	418		202.5	37
P protein	8125	22	383		202.5	36
Drosophila melanog	92E	22	1639		203.5	35
S	406	21	290		203.5	34
	406	21	279		203.5	3
İs		21	279		205.5	32
919		21	263		206.5	31
nila mela	ABB61661	22	412		207	30
		22	272		207.5	29
lococcus a		22	251		207.5	28
S		21	242		210	27
İS		21	240		210	26
S		21	274		211.5	25
ŝ		21	273		211.5	24
Arabidopsis thalia	AAG51431	21	263		211.5	23
bidopsis		21	263		211.5	22
aureus N		22	246		212.5	21
taphylococcus		22	246		214.5	20
		22	246		214.5	19
Staphylococcus aur		22	246		214.5	18
	8	22	246		214.5	17
Staphylococcus aur	AAB15707	21	246		214.5	16
beta-ke	932	17	315	13.7	222.5	15
Rape leaf beta-ket	932	17	315	13.7	222.5	14
conate: NADP+-5	W0211	17	256	13.7	222.5	13
Drosophila melanog	ABB59275	22	257	14.0	227.5	12

ALIGNMENTS

RESULT AAY27004

AAY27004 standard; Protein; 313

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PTXRAX PXXRX PXXXXX PXXXX XXXX XXXX XXXX XXX XXX PXX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondria; immuné disorder; cancer; leukemia; adenocarcinoma; lymphoma; breast; lung; testis; prostate; brain; Addison's disease; acquired immune deficiency syndrome; asthma; anemia; Crohn's disease; Graves disease; AIDS; gene therapy.
                                                                                   WPI; 1999-429503/36.
N-PSDB; AAX86772.
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Nucleic acids encoding human short chain dehydrogenase enzymes

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RESULT
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ID AAB4
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        Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antilinflammatory; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension
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cc which represent the human ORFX open reading frames 1 to 3161. The ORFX cy sequences have activities such as: cytostatic; hepatotropic; vulnerary; cc antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; hepatotropic; vulnerary; cc antipsoriatic; antiparkinsonian; nootropic; neuroprotective; cc antipsoriatic; antiparkinsonian; nootropic; neuroprotective; cc antipsoriatic; hypotensive; dermatological; humunosuppressant; cc antipsoriatic; hypotensive; dermatological; humunosuppressive; dermatological; humunosuppressive; cc antihyroid; and antimaemic. The sequences can be used for determining cc antihyroid; and antimaemic. The sequences can be used for determining cc pathological conditions associated with an ORFX-associated disorder. The notelic acids can be used to express ORFX proteins in gene therapy cretors. The proteins and nucleic acids may be used to treat cancers, coroliferative disorders, neurodegenerative disorders, osteoarthritis, cg graft vs host disease, cardiovascular disease, diabetes mellitus, cc graft vs host disease, cardiovascular disease, diabetes mellitus, cc appertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, cc allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, conocturnal haemoglobinuria, antiinflammatory disease; to enhance cc cagulation; to inhibit thrombosis; and as a contraceptive.
31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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DB; AAC76849.
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99US-0127636.
99US-0127728.
2000US-0540763.
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Query Match Best Local S Matches 312

Local Similarity hes 312; Conserv

Conservative

99.8%;

Score 1619; DB 21; Pred. No. 1.3e-163; 1; Mismatches 0;

Indels Length

0;

Gaps

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Query Match
Best Local Similarity
Watches 312; Conserve
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                                                                                                                                                                                        This invention relates to purified human proteins AAB81047 - AAB81056 which are encoded by cDNA sequences AAF77476 : AAF77485. The invention includes an expression vector which can translate DNA encoding the protein or express it in a cell. Also included is a cell transformed by the vector, and an antibody specific for the protein. The protein can be used for the detection of receptors and ligands and in the screening for new low molecular weight drugs. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; HP00758;
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                     Claim 1; Fig 5;
                                                                                                                                                                                                                                                                                       Novel protein useful for the detection of for screening low molecular weight drugs
                                                                                                                                                                                                                                                                                                                                                                  28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
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                                                                                                                                                                                  protein
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DB; AAF77480.
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vpkwiialytskf 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein HP01017 amino acid sequence
                                                                                                                                                                                 product of
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                     35pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                              low molecular weight drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                 the human cDNA clone HP00758
                                                                                                                         99.8%;
99.7%;
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Pred. No. 1.3e-163;
                                                                                                                Mismatches
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                                                                                                                                 22; Length
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n the screening for
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AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                             Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psorlasis; sepsis; diabetes; atherosclerosis; skin disorder; angiogenic disorder; kidney disorder; cardiovascular disorder; angiogenic disorder; kidney disorder; tumour:
             proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune sys
                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1999;
27-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-2000; 2000WO-US30653.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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cell culture; chemotaxis; food additive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune system disorder; AIDS; autoimmune disease; rheumatoid arthr inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene
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                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    foetal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abnormality; developmental abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein; proliferative disorder; cancer; chromosome
                                                                                                                                                                                                                                                                                                              AAH32600
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                                                                                                                                                                                                                  Page 549; 60fpp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-encoded secreted protein HHFCZ67, SEQ
                                                                                                                                                                                                                                                                                                                                                            Komatsoulis
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2000US-0221193.
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on; wound healing;
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disorder; tumour;
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                                                                                                                                                                                                                                                                                                                                                              Moore
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              system,
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CC anithodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked CC immunosorbent assay (ELISA). The present sequence represents a human xxx entered protein of the invention.
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Best Local Similarity
Matches 144; Conserv
                                                                                                                                                                                                                                                                                       Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDs elmer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; accorder; kidney disorder; promiser; meannancy-related disorder; kidney disorder;
Ruben SM,
                                                                                                       08-NOV-2000; 2000WO-US30653
                                                             12-NOV-1999;
27-JUL-2000;
                                                                                                                                           17-MAY-2001
                                                                                                                                                                          WO200134628-A1
                                                                                                                                                                                                                                                   endocrine disorder; infection; wound heacell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                  gastrointestinal disorder; pregnancy related endocrine disorder; infection; wound healing;
                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene 22-encoded secreted protein fragment; SEQ ID NO:254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG73479 standard; Protein; 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                u
                                                                                                                                                                                                                                          partner
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                                                         99US-0164735
2000US-0221193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                       identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.0%; Score 746; DB 22;
100.0%; Pred. No. 4.6e-71
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                kidney disorder;
disorder; tumour;
                                                                                                                                                                                                                                                                  vulnerary;
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cc and their corresponding secreted proteins are useful for preventing, cc treating or ameliorating medical conditions, e.g., by protein or gene cc therapy. Pathological conditions can be diagnosed by determining the camount of the new protein in a sample or by determining the camount of the new protein in a sample or by determining the presence of cc and include developing products for the diagnosis or treatment of the can include developing products for the diagnosis or treatment of cp proliferative disorders, cancer, tumours, foetal and developmental cambormalities, haematopoietic disorders, diseases of the immune system, abnormalities, neurological disorders (e.g., Alzheimer's disease, cardiovascular disorders (e.g., Alzheimer's disease, cardiovascular disorders, programs), sepsis, diabetes, atherosclerosis, cardiovascular disorders, pregnancy-related disorders, asthma, cc disorders, and infections. The proteins can also be used to aid wound culture of primary tissues, to regenerate tissues, to identify their constated lyands or binding partners; and in chemotaxis, and can be used in diagnostic immunoassays e.g., radiominoassay of the invention can be used in immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA). The present sequence represents a human cc immunoassay (ELISA).
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 47; 604pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 35 human secreted polypeptides, useful preventing, diagnosing and/or treating e.g. cancers, Parkinson disease and diabetic retinopathy
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Best Local
                                                       10-AUG-2001
                                                                         AAG73481;
                                                                                       AAG73481 standard; Protein;
                                                                                                                                 304 WITALYTSKF 313
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118 wiialntskf 127
                                                                                                                                                                        244 NILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSGLGWLASYLPSELRVPK 303
                                                                                                                                                                                                                 193 PGIVOTELLKEHMAKEEVLODPVLKQFKSAFSS-AETTELSGKCV-----VALATDP 243
                                                                                                                                                                     58
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                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                pgilssral---
                                       gene
                                                                                                                                                                                                                                        82;
                                   22-encoded secreted protein fragment,
                                                      (first entry)
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                             22.9%;
                                                                                                                                                                                                -----ssalsnwaqtlsl---cilpclpsppvcvpadp
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                                                                                                                                                                                                                                      6,
                                                                                                                                                                                                                                    Score 371; DB 22;
Pred. No. 2.8e-31;
6; Mismatches 12
                                    SEQ ID NO:256
                                                                                                                                                                                                                                                      Length 127;
                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                 57
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Komatsoulis GA,

Birse CE,

Moore

PA;

Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

ase; rheumatoid arthritis;
Alzheimer's disease;

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CC amount of the new genes. Specific uses are described for each of the CC 2 genes, based on the tissues in which they are most highly expressed, CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoietic disorders, diseases of the immune system, CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, CC altergies, neurological disorders (e.g., Alzheimer s disease, CC garkinsons's disease), cognitive disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC cardiovascular disorders, angiogenic disorders, schizophrenia, asthma, CC disorders, and infections. The proteins can also be used to aid wound CC dealing and epithelial cell proliferation, to prevent skin aging due to constiture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used CC as a food additive or preservative to modify storage properties. CC alleviating symptoms associated with the disorders mentioned above, and CC indiagnostic immunosasay (ELISA). The present sequence represents a human CC secreted protein fragment referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclero cardiovascular disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder; angiogenic disorder; angiogenic disorder; angiogenic disorder; angiogenic disorder; angiogenic disorder; 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angiogenic dis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1999; 99US-0164735.
27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                           Local
partner identification
                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                     22.2%;
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                                                                                                                                                                                                                    Score 361; DB 22; L
Pred. No. 1.3e-30;
Pred. No. 2;
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                                                                                                                                                                                                                                                                                                                                    Length 72;
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S 밁 S

302

PKWITALYTSKF

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Sequence

303

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Query Match
Best Local Similarity
Matches 120; Conserv

Conservative

35;

21.2%;

Score 344; DB 22; Pred. No. 8.4e-28;

Length 303; Indels 102;

Gaps

19

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RESULT
AAB95802
ID AAB9
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                                                         CC to the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide which comprises one of coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5 end complementary to the complementary strand of a polynucleotide which comprises a 5 end complementary to a combination of complementary strand of a polynucleotide which comprises a 3 equence complementary to a coligonucleotide which comprises a 3 equence, where the coligonucleotide comprises at least 15 nucleotides and the combination of complementary full length comprises as selected from those defined in the specification. The primers are useful for synthesising polynucleotides, content of the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and comprises to a content of the component of the comp
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Ishii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and/or diagnosis of the
full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and for the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-2000;
02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:18783.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprises: (a) an oligo-dT primer and an oligonucleotide complementary
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, Sugiyama
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2000JP-0183767.
2000JP-0241899.
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                                             invention
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T, Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the specification. Where a primer set
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A, Nagai K,
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K, Otsuki
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RESULT ANYSORIES ID ANYSORIES ID ANYSORIES ANYSORY ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON ANYSON 
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              Matches
                                       Query Match
Best Local :
                                                                                                                                                                  The invention relates to gene encoding D-arabinitol dehydrogenase, isolated from Bacilius sp. IKD-SA868 strain. The protein can be expressed by standard recombinant methodologies. D-arabinitol dehydrogenase is used as a clinical diagnosing agent for mycosis. The present sequence represents the D-arabinitol dehydrogenase enzyme.
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                              Claim 1; Page 10-11; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                        Arabinitol dehydrogenase gene encoding D-arabinitol useful as a clinical diagnosing agent for mycosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NIPK ) NIPPON KAYAKU
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                                     Local
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DB; AAZ46762, AAZ46763
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              l Similarity
72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 258 AA
                                                                                                                                    258
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dehydrogenase; clinical diagnosis; mycosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0143637.
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                                16.9%;
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    Score 273.5; |
Pred. No. 2.1e
33; Mismatches
  1.1e-20;
nes 87;
                                                 DB 21;
    Indels
                                                 Length
                                                                                                                                                                                                                                                                                                                                                                              dehydrogenase
                                                 258;
  15;
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5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64

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                              AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the protein in the new genes. Specific uses are described for each of the and include developing products for the diagnosis or treatment of and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                     Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; proliferative disorder; cancer; chromosome foetal abnormality; developmental abnormality; haematopoietic disord immune system disorder; AIDS; autoimmune disease; rheumatoid arthrit inflammation; allergy; neurological disorder; AIzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; mastrointeetinal disorder; anglogenic disorder; kidney disorder;
                                                                                                                                                                                              Disclosure; Page 47; 604pp;
                                                                                                                                                                                                                                                                                                               Ruben
                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1999;
27-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endocrine disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human gene 22-encoded secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG73483 standard; Protein; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       culture; chemotaxis; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELRRHGVSCVSLWPGIVQTELLKEHMA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nsvflmskaagkvm1rqgkgsi1n1ssmsgl--ivntpqpqaaynvskagv1mltkslas 178
                                                                                                                                                                                                                                                                                                              , MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ewaphgvrvntiapgymktkltepyfa 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVP----YGVGKAACDKLAADCAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partner
                                                                                                                                                                                                                                                                                                           Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                  99US-0164735.
2000US-0221193.
                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US30653
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                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                         Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pregnancy-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wound healing; vulnerary;
tumours, icc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment,
          foetal and
diseases of
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                                                                                                                                                                                                                                                                                                         Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                         PA
           developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO:258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
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AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammati allergies, neurological disorders (e.g., Alzheimer's disease, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinsons's disease), cognitive disorders, schizophrenia, asthma,

inflammation,

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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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.73485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoletic disorder; foetal abnormality; haematopoletic disorder; immune system disorder; AIDS; autolmmune disorder; disease; rheumatold arthritis; inflammation; allergy; neurological disorder; Alabetmer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psorlasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; ansigned disorder; kidney disorder; kidney disorder; ansigned disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney disorder; kidney di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endocrine disorder; infection;
cell culture; chemotaxis; food
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                                                                                                                                                                                      12-NOV-1999; 99US-0164735.
27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                          08-NOV-2000; 2000WO-US30653.
                                                                                                                                                                                                                                                                                                                                    17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gastrointestinal disorder;
                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 rgv-glc1------lnnkiryshspgaycgrcraehgthiisfnpvre 112
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                                                                              , MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   partner
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                                                                              Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           giogenic disorder; kidney disorder; pregnancy-related disorder; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                              Birse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 267;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                              CE,
                                                                              Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
.1e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                              Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID
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Sequence

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Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy
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Disclosure; Page 47; 604pp; English.

CC AIDS, autolumne diseases (e.g., rheumatoid arthritis), inflammation, (C allergies, neurological disorders (e.g., Alzheimer's disease, eurological disorders (e.g., Alzheimer's disease, cognitive disorders, schizophrenia, asthma, cc skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc cardiovascular disorders, angiogenic disorders, kidney disorders, cc gastrointestinal disorders, angiogenic disorders, kidney disorders, cc disorders, and infections. The proteins can also be used to aid wound company and epithelial cell proliferation, to prevent skin aging due to culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used cas a food additive or preservative to modify storage properties. CC antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and can dispositic immunoassays e.g., radioimmunoassay or enzyme linked company co AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73448 AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the disgnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, 8 AA; proteins they encode. fragments. The genes

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RESULT
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                            Beta-ketoacyl-ACP reductase; Type II fatty acid synthetase;
                                                                                                               Amino acid sequence of a beta-ketoacyl-ACP reductase protein
                                                                                                                                  06-APR-2000 (first entry)
                                                                                                                                                                        AAY54422 standard; Protein; 248
                                                                                                                                                                                                                                                                      170 CDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHWAKEEVLQDPVLKQF-KSAFSSAET 228
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                                                                                                                                                                                                                                                            cdklaadcahelrrhgvscvslwpgivqtellkehmakeevlqdpvlkqvgkgrakeaen
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78.3%;
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                                                                                                                                                                                                                                                                                                           Score 266; DB 22;
Pred. No. 1.6e-20;
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steroselectivity; 4-chloroacetoacteic acid ester; (S)-4-halo-3-hydroxybutyric acid ester; beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductas

reductase;

beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-C
polybeta-hydroxy fatty acid biosynthesis; optically active;

Bacillus subtilis

4-haol-3-hydroxybutyric

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ABS9275
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AC ABB592
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Best Local
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                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 4617
                           pharmaceutical.
                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                ABB59275;
                                                                                                                                                                                                                                                         ABB59275 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constituting Type II fatty acid synthase, or acetoacetyl-CoA reductase constituting the polybeta-hydroxy fatty acid biosynthesis system. The novel method is used to produce optically active 4-haol-3-hydroxybutyric acid ester, with a high purity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1998;
21-OCT-1998;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asymmetrically reducing 4-halo-acetoacetic acid ester or its derivative with beta-ketoacyl-acyl carrier protein reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid ester. The specification describes a method for product (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a Type II fatty acid synthetase. The enzyme has an extremely high reducing activity and steroselectivity towards 4-chloroacetoactein acid ester who provides the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Producing optically pure (S)-4-halo-3-hydroxybutyric
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N-PSDB; AAZ45749.
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98JP-0300178.
99JP-0098205.
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                                                                                                                                                                                                                                                         Protein;
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29.8%;
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Pred. No. 3e-18;
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                                                    AAW02111;
                                                                           AAW02111 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB37737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                        229 TELSGKCVVALATD 242
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                                                                                                                                              235 deasfstgislpvd 248
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11-JUL-2000;
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DB; ABL03378.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                            14.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIVIO or more genes from Drosophila. The invention biology and in elucidating cell signaling and in higher eukaryotes for the development of its and pharmaceutical drugs. The invention requences (ABL16176-ABL30511), expressed DNA 16178, and the conditional drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection reagent for detecting for elucidating cell signalling
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Pred. No. 1.7e-15;
0; Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      257;
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and cell-cell
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WIPO

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Gluconate: NADP+-5-oxidoreductase

06-MAR-1997

(first entry)

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Best Local
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                                   Rape; leaf; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase; plasmid pJR16.2; cDNA library; Escherichia coli; vector; plastid; stroma; transit peptide; cassette; antisense; ollseed; transgenic plant; crop improvement; lipid; metabolic engineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The gluconobacter oxydans gene may be used to transform cells, to produce higher levels of gluconate. Tartaric acid can now be produced without the difficult purification involved in prepn. from tartar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gluconobacter oxydans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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Brassica napus
                        polymer; rapeseed
                                                                                                 Rape leaf beta-ketoacyl-ACP-ketoreductase.
                                                                                                                          13-APR-1996
                                                                                                                                                   AAR89323
                                                                                                                                                                          AAR89323 standard; Protein;
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                                                                                                                                                                                                                                                                                                                 RGHYFCSVYGARLMVPAGQGLIVVISS-----PGSLQYMFNVPYGVGKAACDKLAADC
                                                                                                                                                                                                                                                                                                                                          vtdqdavidgvaalerd-mgpidilinn--agiq----rrapleefsrkdwddlmstnv 120
                                                                                                                                                                                                                                                                                                                                                                   SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL 124
                                                                                                                                                                                                                                                                                                                                                                                            lsgaralvtgasrgigitlakglarygaevvlngrnaesidsagsgfeaeglkastavfd 68
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Pred. No. 5.6e-15;
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                                    metabolic engineering;
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RESULT 1
AAR89322
ID AAR8
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AC AAR8
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AAR89322

Protein;

AAR89322; 13-APR-1996

(first entry)

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Best Local Similarity
Matches 75; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence corresponds to a rape leaf beta-ketoreductase encoded by a cDNA insert in plasmid pJRL6.2 in Escherichia coli XII-Blue. A plastid stroma targeting transit peptide is present. DNA encoding the protein may be inserted in a vector or expression cassette in sense or antisense orientation for expression in an oilseed plant, e.g. for production of transgenic rape plants with low or modified oil content, diversion of metabolism to alternative storage compounds, e.g. starch, protein or engineered polymers, or production of plants with enhanced oil content. The DNA may also be used as a probe to obtain similar genes from other plants. The transit peptide may be used to direct other proteins to leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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DB; AAQ99305.
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                                                                                                                                                                                                           tfggdvskeadveammkta-idawgtidvvvnn--agi----trdtllirmkksgwdev 177
                                                                                                                                                                                                                                              PVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDI 119
                                                                                                                                                                                                                                                                                  avpkvespvvvvtgasrgigkaialslgkagckvlvnyarsakeaeevskgieaygggai 125
                                  VVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG
                                                                   regasrninvnvvcpgfiasdmtaklgedmek----
                                                                                                     HELRRHGVSCVSLWPGIVQTEL----LKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC
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                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                          237
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Query Match Best Local S Matches Rape; seed; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase; plasmid pJRS10.1; cDNA library; embryo; Escherichia coli; vector; plastid; stroma; transit peptide; cassette; antisense; oilseed; transgenic plant; crop improvement; lipid; metabolic engineering; polymer; rapeseed oil. A plastid stroma targeting transit peptide is present. DNA encoding the protein may be inserted in a vector or expression cassette in sense or antisense orientation for expression in an oilseed plant, e.g. for production of transgenic rape plants with low or modified oil content, diversion of metabolism to alternative storage compounds, e.g. starch, protein or engineered polymers, or production of plants with enhanced oil content. The DNA may also Claim 1; Page 15; 29pp; WPI; 1996-105914/11. N-PSDB; AAQ99304. 01-FEB-1996 Key Brassica napus Sequence plastids be used as a probe to obtain similar transit peptide may be used to direct The sequence corresponds to a rape seed beta-ketoreductase encoded by a cDNA insert in plasmid pJRS10.1 in Escherichia coli XL1-Blue. New isolated rape beta-ketoreductase DNA - used to develop plants with lower or higher oil contents or with altered oil compsn. Chase D, (ZENE) ZENECA LTD 20-JUL-1994; 17-JUL-1995; WO9602652-A2 Peptide Rape seed beta-ketoacyl-ACP-ketoreductase. 236 VVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG 287 238 178 126 tfggdvskeadveammkta-idawgtidvvvnn--agi----trdtllirmkksqwdev 179 120 60 66 Local Similarity mes 75; Conserv N NNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCA AAP-MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCV 59 regasrninvnvvcpgflasdmtaklgedmek-idlnltgvflctqaatkimmkkrkgriiniasvvglignigqanyaaakagvigfsktaa PVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDI 119 avpkvespvvvvtgasrgigkaialslgkagckvlvnyarsakeaeevskgieaygggai 125 HELRRHGVSCVSLWPGIVQTEL----LKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC peptide may Elborough 315 AA; Conservative 94GB-0014622 95WO-GB01678 Location/Qualifiers /note= "Transit peptide" be used to direct other proteins to seed ~ 13.7%; Score 222.5; DB 17; Length 315; 25.7%; Pred. No. 7.9e-15; tive 50; Mismatches 108; Indels 59; English. Fentem PA, Slabas AR, genes from other plants. .; .; White A; 59; Gaps 235 237 178 177 9

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> 270 -kilgtiplgrygqpedvag--lveflalspaasyitg 304

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Search completed: July 31, 2002, 15:08:52 Job time: 231 sec

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	poly	n bone mar	Peptide #8053 enco	human se	Human gene 22-enco	Drosophila melanog	Streptomyces colli	Gluconate:NADP+-5-	Pseudomonas aerugi	<pre>3-ketoacyl-ACP red</pre>	magnoliae	tive P. abyss	seed beta-ke	ă.	Pseudomonas aerugi	Drosophila melanog	ຜ	ORFL15 protein inv	cid seque	S. aureus NADPH-de			Staphylococcus aur	taphylococcus	taphylococcus au	coli cel	no aci	inosa	P24 prot	gene 22-	gene 22-enc	gene 22-enc	gene 22-en	Human colon cancer

ALIGNMENTS

mitochondria; immune disorder; cancer; leukemia; adenocarcinoma; mitochondria; immune disorder; cancer; leukemia; adenocarcinoma; lymphoma; breast; lung; testis; prostate; brain; Addison's disease; acquired immune deficiency syndrome; asthma; anemia; Crohn's disease; Graves disease; AIDS; gene therapy.

OS Homo sapiens.

XX
PN US5928923-A.

XX
PD 27-JUL-1999.

XX
PF 05-FEB-1998; 98US-0019216.

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PR 05-FEB-1998; 98US-0019216.

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PR (1NCY-) INCYTE PHARM INC.

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PI Corley NC, Lal P;

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PI Corley NC, Lal P;

Nucleic acids encoding human short chain dehydrogenase enzymes

WPI; 1999-429503/36. N-PSDB; AAX86772.

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RESULT
AAB42640
ID AAB4
XX AAB4
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                                                           vulnerary; antipsoriatio; antiparkinsonian; nootropic; neuroprotect anticonvulsant; osteopathic; antiarhritic; immunosuppressant; card immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antilinflammatory; antiviral; antibacterial; antifungal; antireumatic; antithyroid; antiviral; antibacterial; antifungal; antiviral; antibacterial; antiparkinsonia; antiviral; antiparkinsonia; antiviral; antiparkinsonia; antiparkinsonia; antiparkinsonia; antiparkinsonia; antiparkinsonia; antiparkinsonia; antiparkinsonia; antiparkinsonia; antiparkinsonian; antiparkinsonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for the diagnosis, associated with abnormal e
                                              antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB42640 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                        ORFX ORF2404 polypeptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
313; Conserv
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                                                                                                                                                                                                                                                                                reading frame; ORFX; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
gene therapy; cancer;
ative disorder; osteoa
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 313;
100.0%; Pred. No. 0;
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cancer; proliferative disorder;
osteoarthritis; graft vs host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                       cytostatic; hepatotropic;
nootropic; neuroprotective;
immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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                                  hypertension;
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                                                                                                                                                                                                                                                                                                                                     C AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX Sequences have activities such as: cytostatic; hepatotropic; vulnerary; cantipsoriatic; antiparkinsonian; noctropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; humanosuppressint; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; coantidiabetic; hypotensive; dermatological; immunosuppressive; antibacterial; antiviral; antifungal; antirheumatic; cantitinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cantitinycoid; and antianaemic. The sequences can be used for determining concentration of or predisposition to, or preventing or treating concentrations associated with an ORFX-associated disorder. The concentrative disorders and nucleic acids may be used to treat cancers, conclude; acids can be used to express ORFX proteins in gene therapy concentrative disorders, osteoarthritis, corporative disorders, neurodegenerative disorders, osteoarthritis, corporative disorders, neurodegenerative disorders, osteoarthritis, corporative disorders, combined immunodeficiency (SCID), AIDS, viral, corporative fungal infection, malaria, autoimmune disorders, asthma, concentral or fungal infection, malaria, autoimmune disorders, asthma, concentral or fungal infection, malaria, autoimmune disorders, asthma, concentration, antiinflammatory disease; to enhance
                                                                                                                                                                                               Query Match
Best Local S
Matches 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 3990; 5507pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergy; aplastic anaemia; nocturnal haemoglobin bone damage; cartilage damage; antiinflammatory thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  severe combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; A
cholesterol ester storage; systemic lupus erythematosus; infection
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP
                   194
                                                       134
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                                                                                                                                                                                                                      Local Similarity
                                                                                                                                            LFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMMDDINNVGLRGHYFCSVY 133
GIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALATDPNILSLSGKVL
                                                 2000-602362/57.
                                                                                         GARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAACDKLAADCAHELRRHGVSCVSLWP
                                                                                                                         lfegvdregggrldvlvnnayagvgtilntrnkafwetpasmwddinnvglrghyfcsvy 133
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990S-0127636.
990S-0127728.
20000S-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodeficiency; malaria; autoimmune ic anaemia; nocturnal haemoglobinuria;
                                                                                                                                                                                                                    76.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                               thrombosis;
                                                                                                                                                                                                   0,
                                                                                                                                                                                                                    Score 240; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                               contraceptive
                                                                                                                                                                                                                                     Length
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burn; wour
                                                                                                                                                                                                                                       313;
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                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                  Novel protein useful for the detection of a receptor and a ligand, and for screening low molecular weight drugs \,\cdot\,
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                  Lhe
                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP2001037482-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; HP00758; low molecular weight drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein HP01017 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB81051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB81051 standard; protein; 313
                                                                                                                                                                                                                                                                                                                                 which are
                                                                                                                                                                                                                                                                                                                      includes
                                                 194
                                                                                             134
                                                                                                                   134
    254
                                                                     194
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nes 240; Conservat
                                                                                                                                        74
                                                                                                                                               74 LFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGHYFCSVY 133
                                                                                                                                                                                                                                                         s invention relates to purified human proteins AAB81047 - AAB81056 ch are encoded by cDNA sequences AAF777476 - AAF77485. The invention ludes an expression vector which can translate DNA encoding the received for a cell. Also included is a cell transformed by vector, and an antibody specific for the protein. The protein can be of for the detection of receptors and ligands and in the screening for low molecular weight drugs. The present sequence represents the teln product of the human cDNA clone HP00758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
garlmvpaggglivvisspgslqymfnvpygvgkaacdklaadcahelrrhgvscvslwp
                                                                                                  GARLAVPAGQGLIVVISSPGSLQYMFNVPYGYGKAACDKLAADCAHELRRHGVSCVSLWP 193
                                                                                                                                  lfeqvdreqqgrldvlvnnayagvqtilntrnkafwetpasmwddinnvglrghyfcsvy 133
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                                                                                                                                                                                                                                                                                                                                                                 F1g
                                                                                                                                                                                                                                          313
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0214315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0214315
                                                                                                                                                                                                                                                                                                                                                              35pp; Japanese.
                                                                                                                                                                              76.7%; Score 240; DB 22; 1 100.0%; Pred. No. 2.1e-234; tive 0; Mismatches 0;
                                                                                                                                                                                                     Length
                                                                                                                                                                                 Indels
                                                                                                                                                                                0
                                                                                                                                                                                Gaps
                                                                                         193
                                            253
                                                                   253
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RESULT AAG73423

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CC proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC parkinsons's disease), cognitive disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, disbetes, atherosclerosis, CC cardiovascular disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound the alling and epithelial cell proliferation, to prevent skin aging due to comburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC Alleviating symptoms associated with the disorders mentioned above, and can be used in diagnostic immunoassay or enzyme linked CC immunosorbent assay (ELISA). The present sequence represents a human cc secreted protein of the invention.
                  treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammation; allergy; neurological disorder; Alzhelmer's disease; Parkknson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and their corresponding secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode AAG73449-AAG73519 represent human secreted protein fragments. The genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200134628-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000; 2000WO-US30653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    secreted protein; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 549; 604pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-encoded secreted protein HHFCZ67,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0164735.
2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moore
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Sox

Sequence

162

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Query Match Best Local Similarity

46.0%;

Score 144; DB 22; Pred. No. 1.9e-137;

Length 162;

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AAB95802
ID AABS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 144;
The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to its polynucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                               Claim 8;
                                                                                                                                                                                                       Primer sets for synthesizing polynuc
full-length cDNAs defined in the spe
and/or diagnosis of the abnormality
full-length cDNAs
                                                                                                                                                                                                                                                                                                                    Ota
                                                                                                                                                                                                                                                                                                                                                                     02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2001
                                                                                                                                                                                                                                                                                                     Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95802;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSGKCYVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSGLG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cdklaadcahelrrhgvscvslwpgivqtellkehmakeevlqdpvlkqfksafssaett 78
                                                                                                                                                                                                                                                                                                                Isogai T,
                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                                                  Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                  99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                               ID 18783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                  Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                          2537pp + CD ROM;
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                                                                                                                                                                                                                polynucleotides, particularly the 5602 the specification, and for the detection mality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO:18783.
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                                                                                                                                                                                                                                                                                                 Hayashi K,
A, Nagai K,
                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                       Saito K,
C, Ousuki
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                                                                                                                                                                                                                                                                                                             Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy.
 combination of edined in
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Nucleic acids encoding 35 human secreted preventing, diagnosing and/or treating e. disease and diabetic retinopathy -

polypeptides, useful f g. cancers, Parkinson'

n's

WPI; 2001-329066/34.

Komatsoulis

GA,

Birse

Œ, Z

'n

Moore

Disclosure;

Page 47;

604pp;

English

AAH32522-AAH32627 represent cDNAs corresponding to 35

human secreted

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; proliferative disorder; cancer; chromosom foetal abnormality; developmental abnormality; haematopoletic disorder abnormality; haematopoletic disorder; by the disorder; AIDS; autochmune disease; rheumatold arthring inflammation; allergy; neurological disorder; Alcheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psorlasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; anglogenic disorder; kidney disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                     12-NOV-1999;
27-JUL-2000;
                                                                                                                                                                                                                             08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                    binding partner
                                                                                                                                                                                                                                                                                                                                                   endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotavia; food addition
                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                  culture; chemotaxis; food additive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
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ilarity 100.0%;
Conservative (
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2000US-0221193.
                                                                                                                                                                                                                             2000WO-US30653
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                                                                                                                                                                                                                                                                                                                                    identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                         c disorder;
arthritis;
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CC and their corresponding secreted proteins are; useful for preventing, CC treating or ameliorating medical conditions, e.g., by protein or gene C therapy. Pathological conditions can be diagnosed by determining the CC amount of the new protein in a sample or by determining the presence of CC mutations in the new genes. Specific uses are described for each of the CS genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoletic disorders, diseases of the immune system, CC allergies, neurological disorders (e.g., Albachmer's disease, CC akidovascular disorders, pooritasis), sepais, disbetes; atherosclerosis, CC parkinsons's disease), cognitive disorders, schizophrenia, asthma, CC parkinsons's disease), cognitive disorders, schizophrenia, asthma, CC gastrointestinal disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC sunburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ilgands or binding partners, and in chemotaxis, and can be used a a food additive or preservative to modify storage properties.

CC alleviating symptoms associated with the disorders mentioned above, and immunosorbent assay (ELISA). The present sequence represents a human CC immunosorbent assay (ELISA). The present sequence represents a human CC secreted protein fragment referred to in the disclosure of the invention.
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Best Local S
Matches 49
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12-NOV-1999;
27-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system disorder; AIDS; autoimmune disease; rheumatoid arthr inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; dibetes; atherosclerosis; sepsis; anthogonic disorder; kidney disorder; cardiovascular disorder: angiogenic disorder; kidney disorder; timour.
                                                                                                       08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary;
                                                                                                                                                                                                                                               WO200134628-A1
                                                                                                                                                                                                                                                                                                                                                                                                                         endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene 22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG73483 standard; Protein; 122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein; proliferative disorder; cancer; chromosome 14;
abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                               partner
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99US-0164735.
2000US-0221193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                       2000WO-US30653.
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100.0%; Pred. No.
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kidney disorder; disorder; tumour

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RESULT
AAG73481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 49
immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDs-delmer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder:
                                                                                                              Human; secreted protein; proliferative disorder; cancer; chi foetal abnormality; developmental abnormality; haematopoiet:
                                                                                                                                                                                                                     10-AUG-2001
                                                                                                                                                                                                                                                            AAG73481;
                                                                                                                                                                                                                                                                                                    AAG73481 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 47; 604pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                       170 CDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         12
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                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                           22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                   (first entry)
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100.0%; Pred. No. 2.:
tive 0; Mismatches
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                                                                                                                                   cancer; chromosome 14;
                                                                                                                                                                           SEQ
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CC protein genes, and AAG73346 AAG73448 represent the proteins they encode. CC AAG73449-AAG73519 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing. CC treating or ameliorating medical conditions, e.g., by protein or gene CC amount of the new protein in a sample or by determining the cCC amount of the new genes. Specific uses are described for each of the CC and include developing products for the diagnosed by determining the cCC and include developing products for the diagnosis or treatment of the abnormalities, haematopoietic disorders, diseases of the immune system, and include developing products for the diagnosis or treatment of CC allergies, neurological disorders, ce.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders, de.g., Alzheimer's disease, cc.g. provided to genes, atheroscierosis, CC allergies, neurological disorders, schizophrenia, asthma, cc.g. providers, angiogenic disorders, kidney disorders, cardiovascular disorders, pregnancy-related disorders, atherosclerosis, CC disorders, and infections. The proteins can also be used to aid wound the pathelial cell proliferation, to prevent skin aging due to contact ligands or binding partners, and in chemotaxis, and can be used to althread additive or preservative to modify storage properties. CC allerylating symptoms associated with the disorders mentioned above, and immunosorbent assay (ELISA). The present sequence represents a human cc. immunosorbent assay (ELISA). The present sequence of the invention.
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Best Local :
                                                                                                                                                           Sequence
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                                242 DPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
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27-JUL-2000; 2000US-0221193.
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l dpnilslsgkvlpscdlarryglrdvdgrpvqdylslssv
                                                                         40;
                                                                                       Similarity
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                                                                     Conservative
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                                                                                     12.8%;
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                                                                                    Score 40;
Pred. No.
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                                                                     Mismatches
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                                                                                                    DB 22;
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.s 0;
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RESULT AAG73479

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AAG73479 standard; Protein; 127

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Sequence

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cc and their corresponding secreted proteins are useful for preventing, ct treating or ameliorating medical conditions, e.g., by protein or gene ct therapy. Pathological conditions can be diagnosed by determining the camount of the new protein in a sample or by determining the presence of comparison of the new genes. Specific uses are described for each of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the comparison of the compariso
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 47; 604pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1999; 99US-0164735.
27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene 22-encoded secreted protein fragment,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pregnancy-related disorder; tumour; on; wound healing; vulnerary.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides, useful for g. cancers, Parkinson's
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haematopoietic disorder;
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Query Match Best Local :

12.8%;

Score Pred.

40; . No.

DB 22; 3e-32;

Length

Local

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                                        CC AAH32527-AAH32627 represent cDNAs corresponding to 35 human secreted CC protein genes, and AAG73346-AAG73448 represent the proteins they encode. CC AAG73449-AAG73519 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, CC treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the presence of mutations in the new protein in a sample or by determining the presence of CC mutations in the new genes. Specific uses are described for each of the CC amount of the new genes. Specific uses are described for each of the CC genes, based on the tissues in which they are most highly expressed, CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC allors autcommune diseases, cancer, the diagnosis of the immune system, CC allergies, neurological disorders (e.g., Alzheimer's disease, asthma, asthma, asthma, asthma, asthma, asthma, asthma, asthma, cCC skin disorders (e.g., psoriasis), sensis, disheres, athercalercies
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                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-2000; 2000WO-US30653
            skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders,
                                                                                                                                                                                                                                                                                                                                                                       disease
                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-329066/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1999; 99US-0164735.
27-JUL-2000; 2000US-0221193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200134628-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene 22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG73482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG73482 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MS
                                                                                                                                                                                                                                                                                                                                                                       c acids encoding :
ting, diagnosing a
e and diabetic re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partner identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komatsoulis
                                                                                                                                                                                                                                                                                                                                      Page 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental abnormality;
                                                                                                                                                                                                                                                                                                                                  604pp;
                                                                                                                                                                                                                                                                                                                                                                       retinopathy
                                                                                                                                                                                                                                                                                                                                                                                    35 human secreted polypeptides, useful for and/or treating e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pregnancy-related disorder; tumour;
on; wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birse CE,
pregnancy-related disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,NO:257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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888888888888888
                                        disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention.
Sequence
28
AA,
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                                         δÃ
                                                                    Query Match
Best Local
                                                            Matches
                                242 DPNILSLSGKYLPSCDLARRYGLRDVDG 269
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                          ᆫ
                        dpnilslsgkvlpscdlarryglrdvdg 28
                                                          ch 8.9%;
1 Similarity 100.0%;
28; Conservative
                                                           0,
                                                                   Score 28;
Pred. No.
                                                            Mismatches
                                                                    1.1
                                                                   .2e-20;
                                                                            22;
                                                                          Length
                                                           Indels
                                                           0
                                                           Gaps
                                                           0
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RESULATION AND SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psorlasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200134628-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; proliferative disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG73488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             partner identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        占
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome 14;
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08-NOV-2000; 2000WO-US30653

12-NOV-1999; 27-JUL-2000; 2000US-0221193 9908-0164735

(HUMA-) HUMAN GENOME SCI INC

, MS Komatsoulis GA, Birse CE, Z 'n Moore

WPI; 2001-329066/34

Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -

Disclosure; Page 47; 604pp; English

AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73448 represent the proteins they encode AAG73449-AAG73449 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing,

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CC treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the CC amount of the new protein in a sample or by determining the CC mutations in the new genes. Specific uses are described for each of the CC and include developing products for the diagnosis or treatment of the CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC proliferative disorders, cancer, tumours, foetal and developmental CC alboryless, neurological disorders, diseases of the immune system, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC allergies, neurological disorders, schizophrenia, asthma, CC exin disorders (e.g., psorials), sepsis, diabetes, atherosclerosis, CC gastrointestinal disorders, anglogenic disorders, schizophrenia, asthma, CC cardiovascular disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC culture of primary tissues, to regenerate tissues, to identify their CC cas a food additive or preservative to modify storage properties.

CC alleviating symptoms associated with the disorders; mentioned above, and cc in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                     in diagnostic immunoassays e.g., radioimmunoassay or enzyme limmunosorbent assay (ELISA). The present sequence represents secreted protein fragment referred to in the disclosure of the
                                                                                                                                                                                                                           24 AA;
                  100.08; **
                                                                Score 24; Pred. No.
                          Mismatches
                                                        DB 22;
1.1e-16;
                                                                                                                                                                                                                                                     disclosure of the invention
                                                                               Length 24;
               Indels
       0;
                                                                                                                                                                                                                                                                                                  human
0;
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expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The color cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. When a proper a prevention, diagnosis and treatment of diseases associated with inappropriate production.

The colon

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.

present for

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                                                                                                               Ş
                                                                                                                              Matches
                                                            73927
Human colon cancer antigen protein SEQ ID NO:4691.
                        03-SEP-2001
                                                  AAG73927 standard; Protein; 127
                                                                                         Local Similarity 100.
les 24; Conservative
                    (first entry)
                                                    B
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δÃ 밁

218 QFKSAFSSAETTELSGKCVVALAT 241

88 qfksafssaettelsgkcvvalat 111

Matches Query Match Best Local

24;

Similarity 100. 24; Conservative

100.0%; 7.78;

0;

Mismatches

4.8e-16; DB 22;

Length 127;

Indels

0;

Gaps

0

Score 24; Pred. No.

Local

Sequence

127 AA;

RESULT 13

AAG73486 standard; Protein; 127

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WO200122920-A2
                                                Homo sapiens
                                                   Human; colon cancer; colon cancer antigen; diagnosis; detection;
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Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoietic disorder; inflammation; allergy; neurological disorder; Albeiner; altergy; parkinson's disease; cognitive disorder; Altheiner's disease;

Human gene 22-encoded secreted protein fragment,

SEQ ID

NO:261

10-AUG-2001 AAG73486;

(first entry)

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colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                Nucleic acids encoding 35 human secreted polypeptides, useful for
                                                                                         12-NOV-1999;
27-JUL-2000;
                             WPI; 2001-329066/34.
                                                     Ruben
                                                                                                                   08-NOV-2000; 2000WO-US30653
                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                              WO200134628-A1
                                                                                                                                                                                                        endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                     skin disorder; psoriasis; sepsis; diabetes; athizophrenia; asthma; cardiovascular disorder; appoies; diabetes; atherosclerosis; gastrointestinal disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder;
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                       binding
                                                                                                                                                                                                                              gastrointestinal disorder;
                                                     ,MS
                                                                                                                                                                                                     partner
                                                Komatsoulis
                                                                                       200005-0221193.
                                                                                                  9908-0164735
                                                                                                                                                                                                   identification
                                                 GA,
                                              Birse CE,
                                                                                                                                                                                                                 pregnancy-related
on; wound healing;
                                              Ľ
                                         Moore
                                                                                                                                                                                                                        disorder; tumour;
                                                                                                                                                                                                                                  kidney disorder;
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Claim 11; Page 6490-6491; 9803pp; English.

Nucleic acids encoding useful for preventing,

y 4277 human diagnosing

WPI; 2001-235357/24. N-PSDB; AAH33358.

Ruben

, MS

Barash SC,

Birse CE,

Rosen CA;

(HUMA-) HUMAN GENOME

SCI INC.

29-SEP-1999; 03-NOV-1999;

99US-0157137. 99US-0163280.

28-SEP-2000; 2000WO-US26524.

05-APR-2001

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AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, callergies, neurological disorders (e.g., Alzhelmer's disease, allergies, neurological disorders (e.g., Alzhelmer's disease, cognitive disorders, schizophrenia, asthma, cc skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc cardiovascular disorders, angiogenic disorders, kidney disorders, cc gastrointestinal disorders, pregnancy-related disorders, endocrine cc disorders, and infections. The proteins can also be used to aid wound the company and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell cc culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Cc antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and can include assay (ELISA). The present sequence represents a human cc secreted protein fragment referred to in the disorders of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode AAG732449-AAG73519 represent human secreted protein fragments. The genes
                                                                                                                                                                                        Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder;
                  WO200134628-A1
                                                                                                                         endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                     gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                  10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG73484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG73484 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preventing,
disease and
                                                                                                                                                                                                                                                          inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 QFKSAFSSAETTELSGKCVVALAT 241
                                                                                                                                                                                                                                                                             mmune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  their corresponding secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qfksafssaettelsgkcvvalat 111
                                                                                                                                                                                                                                                                                                 secreted protein; proliferative disorder; cancer; chromosome 14; abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                       partner identification
                                                                                                                                                                                                                                                                                                                                                                    22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosing and/or treating e.g. cancers, Parkinson's diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 24;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                              pregnancy-related disorder;
on; wound healing; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 127;
                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO: 259
                                                                                                                                                                        tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc and include developing products for the diagnosis or treatment of cc and include developing products for the diagnosis or treatment of cc proliferative disorders, cancer, tumours, foetal and developmental cc abnormalities, haematopoietic disorders, diseases of the immune system, cc allergies, neurological disorders (e.g., rheumatoid arthritis), inflammation, cc allergies, neurological disorders (e.g., Alzheimer's disease, cancer (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc cardiovascular disorders, anglogenic disorders, xidney disorders, cc cardiovascular disorders, anglogenic disorders, xidney disorders, cc cardiovascular disorders, pregnancy related disorders, andocrine cc disorders, and infections. The proteins can also be used to aid wound cc disorders, and organs before transplantation, for supporting cell cc culture of primary tissues, to regenerate tissues, to identify their cc cognate ligands or binding partners, and in chemotaxis, and can be used cas a food additive or preservative to modify storage properties.

Cc Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and consisting furning sense of a redicing management linked and consisting symptoms associated with the disorders mentioned above, and consisting symptoms associated with the disorders mentioned above, and consisting the sense of the disorders mentioned above, and consisting symptoms associated with the disorders mentioned above, and consisting symptoms associated with the disorders mentioned above, and consisting symptoms associated with the disorders mentioned above, and consisting symptoms associated with the disorders mentioned above, and consisting symptoms associated with the disorders mentioned above.
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Matches 20
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Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amount of the new protein in a sample or by determining mutations in the new genes. Specific uses are described
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                                                                           Human gene 22-encoded secreted protein fragment,
                                                                                                                              10-AUG-2001
                                                                                                                                                                                   AAG73487;
                                                                                                                                                                                                                                    AAG73487 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention
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and their corresponding secreted protein iragments. The genes treating or ameliorating medical conditions, e.g., by protein or gene camount of the new protein in a sample or by determining the correct the new protein in a sample or by determining the correct the new protein in a sample or by determining the correct to the new protein or gene and include developing products for the diagnosed by determining the correct proliferative disorders specific uses are described for each of the correct tenders, they are most highly expressed, allergies, haematopoietic disorders, foetal and developmental correct tumours, foetal and developmental correct tumours, foetal and developmental correct tenders, diseases of the immune system, allergies, neurological disorders (e.g., Alzheimer's diseases, capitive disorders, diseases, contributed arthritis), inflammation, correct standards disorders, scandards arthritis), inflammation, correct standards and infections. The proteins can also be used to aid wound contribute of primary tissues, to regenerate tissues, to deentify their compate ligands or binding partners, and in chemotaxis, and can be used in diagnostic immunosassays e.g., radioimmunosassay or enzyme linked in disorders mentioned above, and can be used in diagnostic immunosassays e.g., radioimmunosassay or enzyme linked in the disorders mentioned above, and secreted protein fragment referred to in the disorders of the invention.
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47; 604pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
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27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding partner identification.
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Matcheg

Conservative

5.8%; Score 18; 100.0%; Pred. No. ative 0; Mismatc

DB 22; le-10;

22; Length 18;

Mismatches

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Indels

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Search completed: July 31, 2002, 15:13:33 Job time: 232 Sec

ΧX

Run on: OM protein -

July 31,

protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Com

Compugen.Ltd.

Maximum Minimum

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     of hits satisfying chosen parameters:
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2: sp_bacteria
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1623
                                                       562222 seqs, 172994929 residues
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1795.934 Million cell updates/sec
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Q96LJ7
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Q96b59 homo sapien
Q96cq5 homo sapien
Q99104 mus musculu
Q9d148 mus musculu
Q9n538 caenorhabdi
Q16764 caenorhabdi
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054118 streptomyce
09kfr7 bacillus ha
098ge0 rhizobium 1
09ewt2 streptomyce
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                                             Q912r7 pseudomonas
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Q96LJ7;
Q15LJ7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25430 FIS, CLONE TST06262.
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OShima A., Takahashi-Fujii A., Tanase T
Oshima A., Takahashi-Fujii A., Hara
Arita M., Musashino K., Yuuki H., Hara
Arita M., Misuno S., Morinaga M., Ka
Irie R., Otsuki T., Sato H., Nishikawa
Nagai K., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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Result No.

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248	246	257	246	278	254	251	374	328	254	254	320	315	273	271	258	255	272	254	270	257	268	253	247	261	249	266	266	249
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Q97FV0	Q99QK7	Q987C7	Q9KA03	Q9A3M7	Q9RH24	Q98FG6	Q989M0	Q93X67	Q949M2	Q95PA3	Q93X62	Q949M3	Q9F5J1	032336	Q92TX5	Q9APX4	Q9SQR2	Q95PA6	Q9SQR4	Q9VNF3	Q9HLN6	Q9K3Y7	Q92AK1	Q9FK50	Q97DA6	Q9HWN3	Q03906	Q9KEB5
Q97fv0 clostridium		Q987c7 rhizobium l		Q9a3m7 caulobacter	Q9rh24 zymomonas m		Q989m0 rhizobium l	Q93x67 brassica na	brass	edes aegy	Q93x62 brassica na	Q949m3 brassica na	Q9f5jl streptomyce		Q92tx5 rhizobium m		N		4	Ω	Q9hln6 thermoplasm	Ø				ω	Œ	Q9keb5 bacillus ha

ALIGNMENTS

RI NABOA K., ISOGAL T., SUGANO S.; RI NABOA MINAN CONA SEQUENCING POJECT. "; RI SUDMITTED (CCT-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL; AKOS8159; BAB71694.1; SQ SEQUENCE 313 AA; 33909 MW; 832F83FA75D931A3 CRC64; Query Match 99.8%; Score 1619; DB 4; Length 313; Best Local Similarity 99.7%; Pred. No. 1.2e-133; Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Matches 312; Conservative 1; Mismatches 0; Indels 0; Gaps 0 Qy 1 MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVP 60
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Tanase T., Imose N.,

Takeuchi K.,

Hara H., Suzuki Y., Hata H., M., Kawamura M., Sugiyama T.,

Sugiyama A., Kawakami B.,

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RESULT 3
Q96CQ5
ID Q96CQ5
AC Q96CQ5;
DT 01-DEC-2001 (
DT 01-DEC-2001 (
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Best Local Similarity 99.4
                                                                                                                                                 301 VPKWIIALYTSKF 313
                                                                                                                                                                                                   181 LRRHGVSCVSLWPGIVOTELLKEHWAKEEVLODPVLKOFKSAFSSAETTELSGKCVVALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ, databases.
EMBL; BC015943; AAH15943.1;
Hypothetical protein.
SEQUENCE 313 AA; 33881 MW; ED0D252724E38776 CRC64;
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PRELIMINARY;
PRT; 313 AA.

Q96B59;
Q1-DEC-2001 (TremBLrel. 19, Created)
Q1-DEC-2001 (TremBLrel. 19, Last sequence update)
Q1-DEC-2001 (TremBLrel. 19, Last annotation update)
HYPOTHETICAL 33.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-MELANOMA;
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Bukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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301 VPKWIIALYTSKF 313
                                                                                                                                                                                                                LRRHGVSCVSLWPGTVQTELLKEHMAKEEVLQDPVLKQFKSAPSSAETTELSGKCVVALA 240
                                                                                                                                                                                                                                                   NVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAACDKLAADCAHE
                                                                                                                                                                                                                                                                                               NVGLRGHYFCSVYGARLMVPAGOGLIVVISSPGSLQYMFNVPYGVGKAACDKLAADCAHE 180
                                                                                                                                                                                                                                                                                                                                                 MAAPMNGQACVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVP
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                                                           PRELIMINARY;
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            Created)
Last sequence update)
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Catarrhini; Hominidae; Homo.
                                                       313
                                                    AA.
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Q99L04;
Q99L04;
O1-JUN-2001 (TrEMBLrel. 17, Cr
O1-JUN-2001 (TrEMBLrel. 17, Lc
O1-DEC-2001 (TrEMBLrel. 19, Lc
RIKEN CDNA 1110029G07 GENE.
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                                         EMBL; BC003930; AAH03930.1; MGD; MGI:1915960; 1110029607Rik. InterPro; IPRO02198; ADH_short.
                                                                          Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                           Strausberg R.;
                                                                                                                                          TISSUE
                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                     TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL.
                                                                                                                                                                                   NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   1110029G07RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LRRHGVSCVSTMPGIVQTELLKEHMAKEEVLQDDVLKQFKSAFSSAETTELSGKCVVALA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-PANCREATIC ADENOCARCINOMA;
Strausberg R.;
Strausberg (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC014057; AAH14057.1; -
SEQUENCE 313 AA; 33925 MW; 37FA022675C4F076 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NYGLRGHYFCSVYGARLMYÞAGQGLIVVISSÞGSLQYNFNYLYGVGKAACDKLAADCAHE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              Α
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        34005 MW;
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99.48;
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, Last sequence up
, Last annotation |
60E05BD7911BDC0C CRC64;
                                                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae
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Pred. No. 8.9e-133;
1; Mismatches 1;
                                                                                                                                                                                                                                             sequence update;
annotation update;
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                                                                                                                                  7 MONTHS
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240

120

Indels.

0, Gaps

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241

241 181 181 121

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Query Match Best Local Similarity

85.7%; 82.4%;

Score 1391; DB 11; Pred. No. 1.1e-113;

Length Indels

313;

Gaps

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258;

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27;

Mismatches

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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Besole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shbata Y., Storch K.-F.,
Saka Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Hayashtaki P., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Hayashtaki M., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q9D148;
01-JUN-2001
"Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
EMBL; AK003958; BAB23093.1; -
MGD; MGI:1919560; 1110029507R1k.
SEQUENCE 313 AA; 34031 MW; 80E8ECD7910EDC03 CRC64;
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Mammalia; Eutheria;
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(TrEMBLrel. 17, Last sequence up)
(TrEMBLrel. 19, Last annotation)
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Rodentia;
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Query Match Best Local Similarity

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Score 1370; DB 11; Pred. No. 7.6e-112;

Length

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Holmes A., Elliot G., Cloud J.;
"The sequence of C. elegans cosmid Y32H12A.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                EMBL; AC006733; AAF60486.1; -. HSSP; P50162; 1AE1. InterPro; IPR002198; ADH_short.
                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
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                                                                                         PRINTS; PRO0080; SDREAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
Hypothetical protein; Oxidoreductase.
SEQUENCE 319 AA; 35067 MW; F6B5DDAE07EE734E CRC64;
                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2; MEDLINE-99069613;
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  43.7%;
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InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
Hypothetical protein; Oxidoreductase.
SEQUENCE 323 AA; 35824 MW; 4FE24D30ED39CAE3 CRC64;
                                                                                                                                                                                          "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-TAN-1998 (TrEMBLrel. 05, Created)
Ol-TAN-1998 (TrEMBLrel. 05, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 35.8 KDA PROTEIN.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99089613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                    Bradshaw H.;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a poinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                 Submitted
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                                                                                                                                                                                                                                                                                                                            sequence of C. elegans
itted (AUG-1997) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPSFLRVPKWII 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSLASDPRRMDKTGRILITEDLGKEYGFYDIDGLRPPNLRSVSFILKH----LGWNTTANF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOVCVVTGASRGIGRGIALQLCKAGATVYITGRH-------LDTLRVVAQEAQSLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146;
                                                                                                                                                                                      FAMILY.
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
 37.9%; Score 615; DB 5;
42.1%; Pred. No. 1.1e-45;
Live 58; Mismatches 112
                                                                                                                                                                                                                                                                                                                        cosmid F59E11.";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
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                                    Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                             platform for ng Consortium.";
   Indels
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 20;
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Gaps
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                                                                                                Query Match
Best Local S
Matches 130
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                         Local Similarity
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5 MNGQVCVVTGASRGIGR----GIALQLCKAGATVYITGR---

Indels

36;

Gaps

5

---HLDTLRVVAQ 49

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"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES,
(SDR) FAMILY.

R EMBL; U41018; AAA82327.1; --
R InterPro; IPR002198; ADH_short.
R Pfam; PF000106; adh_short; 1
R PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.

R PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.

W Hypothetical protein; Oxidoreductase.
SEQUENCE 325 AA; 35919 MW; D68C60E9105AE177 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Nhan M., Leimbac D.;
"The sequence of C. el
Submitted (DEC-1995) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q23612
Q23612;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a pinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 35.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZK816.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGLGWLASYLPSFLRVPKWIIALYTSKF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARMSTDMAVELNPYNYCVYTLIPGPYKTETANRTIIDDAYKMIKENPELEE----FIKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITSRGGKGIALYVDHSNMTEVKFLFEKIKEDEEGKLDILVNNVYNSLGKATEMIGKTFFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGKEEVAKYIPPQIKLPKWVIWQSVNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEYTGKALARLAMDPGKLKKSGKTLFTEDLAQKYDFSDKHGAGMEPQNIRSIRTILG-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTELSGKCVVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPV--QDYLSLSSVLSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPASMWDDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAAC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQSLGGOCVPVVCDSSQESEVRTLFEQVDREQOGRLDVLVNNAYAGVQTILNTRNKAFWE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGVILQDQVALVTGASRGIGRGIALQLGEAGATVYITGRRPELSDNFRLGLPSLDYVAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                        , elegans
5) to the
                      35.9%;
39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nematoda;
                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ databases.
TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oda; Chromadorea;
Caenorhabditis.
Score 583; DB 5;
Pred. No. 6.8e-43;
5; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                    cosmid ZK816.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhabditida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            platform for
                                       Length 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhabditoidea;
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       문
                                                                                                 Matches
                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O54118 PRELIMINARY;
O54118;
01-JUN-1998 (TrEMBLrel. 0
01-JUN-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                       Oxidoreductase.
                                                                                                                                                                                                                                                   (SDR) FAMILY.

EMBL; ALO21529; CAA16459.1; -.

InterPro; IPR002198; ADH_short.

Pfam; PP00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapaite D.,
Kinashi H., Hopwood D.A.;
*A set of ordered cosmids and a detailed
the 8 Mb Streptomyces coelicolor A3(2) ch
Mol. Microbiol 21:77-96(1996).
-1- SIMILARITY: BELONGS TO THE SHORT-CHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy L., Harris D.;
Submitted (JAN-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SC10A5.27C PROTEIN SC10A5.27C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
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                                  PMNGQVCVVTGASRGIGRGIALQLCKAGATVYIT------GRHLDTLRVVAQEAQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLS-LAGYHSMAGWCPEWVNLPGWAITLWQNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --FLNGESTEYCGKAVVAIAADPKKKYWNGSTLITTDMGNYYSYTDIDGRIPTNMRQLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERDPEIWDDINNVGLRNQYYCSVYGTRIMRKNGMKGLIVNISSLGGIMYLFTVAYGVGKM
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                                                                                                                         Similarity
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J., Barrell B.G., I
(JAN-1998) to the
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                                                                                              Conservative
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e EMBL/GenBank/DDBJ
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                                                                                            Score 347.5; DB 2
Pred. No. 2.9e-22;
5; Mismatches 102
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Q9KFR7;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID-86665;
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Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome; SEQUENCE 302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                          SAFSSAETTELSGKCVVALATDPNILSLSGKVLPSCDLARRYGLRDVDG
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PHFVISESPRFVGRAVAALASDPNVSRWNGQSLSSGQLAQAYGFTDLDG
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                                                                                                                            -YGVGKAACDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM-AKEEVLQDPVLKQFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94;
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33422 MW; CEl3F300140D55BB
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22.58;
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ús group; Bacillus:
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DNA Res. 7:331-338(2000).
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Phyllobacteriaceae; Mesorhizobium.
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C912R7,
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (DECTORAIN DEHYDROGENASE.
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-ARCC 15692 / PAO1;

MEDLINE-20437337; Pubmed-10984043;

MEDLINE-20437337; Pubmed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                               Pseudomonas
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a
the 8 Mb Streptomyces coelicolor A3(2) chromosome.
Mol. Microbiol. 21:77-96(1996).
EMBL; AL449216; CAC14941.1;
SEQUENCE 308 AA; 33485 MW; D7BD8D12D812832B CF
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A Jones L.-M., Kaerst U., Kreft J., Kunh M., Kunst F., Kurapkat G.,
A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
A Nordslek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Nordslek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Nordslek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Nordslek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Nordslek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Comparative genomics of Listeria species.";
C. Science 294:849-852(2001).

BELL, ALS96170; CAC97027.1; -.
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PROSITE; PS00061; ADH_SHORT; 1.
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"Complete genome sequence of
opportuniatic pathogen.":
Nature 406:959-964(2000).
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Maier M.H., Hancock R.E.W., 1
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Lory S., Olson M.V.;
s aeruginosa PAO1, an
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                                                                                                                                                       EMBL; 284498; CABO6498.1; --
HSSP; P50163; 2AE1.
TubercuList; Rv1928c; --
InterPro; IPR002198; ADH_short.
InterPro; IPR003013; HLH_Myc.
Pfam; PF00106; adh_short; 1.
                                                Piam; Froncesons SDRFAMILI.

PRINTS; PRO0080; SDRFAMILI.

PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

Complete proteome; Hypothetical protein; Oxidoreductase.

Complexe 255 AA; 27031 MW; 454692E6FAA253FF CRC64;
                                                                                                                                                                                                                                                                                                                   MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H. Gordon S.V., Eiglmeier K., Gas S., Barry.C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hol Davies R., Devlin K., Krogh A., McLean J., Moule S., Murphy Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy Hornsby T., Seborne J., Quall M.A., Rajandream M.A., Rogers J. Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from t
                                                                                                                                                                                                                                                                    "Deciphering the biology of Mycobacterium complete genee sequence.", Nature 393:537-544 (1998)."
-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P95286 PRELIMINARY; PRT; 255 AA. P95286; O1-MAY-1997 (TrEMBLrel. 03, Created) O1-MAY-1997 (TrEMBLrel. 03, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat HYPOTHETICAL 27, 0 KDA PROTEIN. RV1928C OR MTCY09F9.36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Pred. No. 4.3e
%6; Mismatches
Score 271; DB pred. No. 1e-1
97; Mismatches
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MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64

Matches

Similarity

Conservative

37;

1e-15;

.83

Indels

14;

Gaps

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: July 31, 2002, 15:05:36 ; Search time 17.53 Seconds (without alignments)
1715.885 Million cell updates/sec

Title: Perfect score: Sequence: US-10-006-163-1 1623 1 MAAPMNGQVCVVTGASRGIG......YLPSFLRVPKWIIALYTSKF 313

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283138

283138 seqs, 96089334 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database : Post-processing: Minimum Match 0% . Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	ဖ	8	7	6	υī	4	ω	2	<u>, </u>	Result No.	
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3-oxoacyl-(acyl-ca 2-deoxy-D-gluconat	protein F14N23.19	3-oxoacyl-(acyl-ca	oxidoreductase,	short-chain alcoh	2-deoxy-D-gluconat	2-deoxy-D-gluconat	probable sterol d	3-oxoacyl-[acyl-c	probable short-che	probable 3-ketoacy	3-oxoacyl-(acyl-c	3-oxoacyl-[acyl-c	3-oxoacyl-(acyl-ca	short chain dehydı

ALIGNMENTS

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Qy 279 SSVLSHVSGLGWLASYLPSFLRVPKWIIAL 308 :: : : Db 310 PTLRKHSWLIPD-IKVP-WSILL 330	Qy 227 ETTELSGKCVVALATDPNILSLSGKVLPSCDLARRYGLRDVDGR-PVQDYLSL 278	Qy 171 DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFK-SAFSSA 226	Qy 111 TPASMWDDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAAC 170	51 AOSLGGOCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWE	Qy 5 MNGQVCVVTGASRGIĞRGIALQLCKAGATVYITGRHLDTLRVVAQE 50 : : : : : : : : : : : : :	Query Match 38.0%; Score 617.5; DB 2; Length 339; Best Local Similarity 43.0%; Pred. No. 1e-42; Matches 142; Conservative 53; Mismatches 94; Indels 41; Gaps 12;	RESULT 1 AE2212 Appothetical protein alr3252 [imported] - Anabaena sp. (strain PCC 7120) C;Species: Anabaena sp. C;Shecies: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AE2212 C;Accession: AE2212 R;Kaneko, T; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irig Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Accession: AE2212 A;Status: prelinninary A;Molecule type: DNA A;Residues: 1-339 <kur> A;Cross-references: GB:BA000019; PIDN:BAB74951.1; PID:g17132347; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics: C;Genetics:</kur>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-325 <NHA>
                                                                                                    A; Introns: 24/1;
                                                                                                                                   A;Cross-references: EMBL:U41018; PIDN:AAA82327.1; CESP:ZK816
                                                                                                                                                                                                              A; Reference number:
A; Accession: T29604
                                                                                                                                                                                                                                   submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid ZK816.
                                                                                                                                                                                                                                                                                                       hypothetical protein ZK816.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #teC;Accession: T25964
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                                                                                 ;Gene: CESP:2K816.5
;Introns: 24/1; 111/3; 170/2; 228/3; 280/1
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A; Molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 20/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-323 <BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F59E11.
A;Reference number: Z21124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T32125

hypothetical protein F59E11.2 - Caenorhabditis elegans
c;Speciles: Caenorhabditis elegans
c;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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Best Local Similarity
                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         296
                                                                                                                                                                                                                                                                                                                                                                                                                                                286 SGLGWLASYLPSFLRVPKWIIALYTSKF 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ARMSTDMAVELNPYNVCVVTLIPGPVKTETANRTIIDDAYKMIKENPELEE----FIKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM----AKEEVLQDPVLKQFKSAFSSAE 227
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                                                                                                                                                                                                                                                                                                                                                                                                                           MGKEEVAKYIPPQIKLPKWVIWQSVNRF 323
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                           35.98;
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                 55;
                       Score 583; DB 2;
Pred. No. 6.3e-40;
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Pred. No. 1.5e-42;
          Mismatches
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          111;
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      Indels
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     36;
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RESULT
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A; Residues: 1-326 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Murphy, L.; Harris, D.; Parkhill, submitted to the EMBL Data Library, A; Reference number: Z21548
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T34594
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                                                                                    219
                                                                                                                  192
                                                                                                                        160 NVPYGVGKAACDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM-AKEEVLQDPVLKQ 218
                                                                                                                                                                            140
                                                                                                                                                                                   111 TPASMWDDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISSP------GSLQYMF 159
                                                                                                                                                                                                                                       82
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                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 LLS-LAGYHSMAGWCPEWVNLPGWAITLWQNK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 --FLNGESTEYCGKAVVÁIAADÞKKKYWNGSTLITTDMGNYYSYTDIDGRIPTNMRQLRG 291
                                                                                                                                                                                                                                                                                                        4 PMNGQVCVVTGASRGIGRGIALQLCKAGATVYIT------GRHLDTLRVVAQEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 VLSHVSGLGWLASYLPSFLRVPKWIIALYTSK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 SAFSSAETTELSGKCVVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
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                                                                                                                                                                                                                                                                                                                                                                                                                          SCOEDB:SC10A5.27c
                                     --PTFAIAESPHYLARTVAALAADPDRAKRWNGKSTSSGELARAYGVTDVDGSRP
                                                          FKSAFSSAETTELSGKCVVALATDPN-ILSLSGKVLPSCDLARRYGLRDVDG-RP 271
                                                                                                                                                       TPLADGLRILELGARSH----VITAALLLP----LLIRSDAPLHVEVTDGTAHSNRRYRE
                                                                                              NIYYDLAKNAPIRLAFGLAQELABYEGTAVAVSPGFLRSEOMLSHFGVSEENWRDAIAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                            SLGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTR--NKAFWE 110
                                                                                                                                                                                                                                                                            PLAGRIALVAGATRGAGRAQAVELGRAGATVYVTGRTTRARASEVGRTTETIEETAELVT
                                                                                                                                                                                                                 AAGGTGIAVPTDHLDEAQVRALVERIDREYE-RLDILVNDLWGG-EHLLATSVFGKKSWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALDRMSSDMAQELQDTGTTVISLWPSAVKTELITNMIETSAGSWGATENKM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM-----AKEEVLQDPVLKQFK 220
                                                                                                                                                                                                                                                                                                                                                        99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERDPEIWDDINNVGLRNQYYCSVYGTRIMRKNGMKGLIVNISSLGGIMYLFTVAYGVGKM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETPASMMDDINNVGLRGHYFCSVYGARLMVPAG-QGLIVVISSEGSLQYMFNVPYGVGKA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECRKRGGICHVRYVDHSNMDEVEKFFDEVASETDNQLDILVNNAFSAVTKCGSGDTRKFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAQSLGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFW 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKSKIAIVTGASRGCGRGMLKGVALQLAEAGCTLYITGRAPSKTLSSELTYLPTLEGTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNGQVCVVTGASRGIGR----GIALQLCKAGATVYITGR----
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:AL021529; PIDN:CAA16459.1; ce: strain A3(2)
                                                                                                                                                                                                                                                                                                                                          21.4%; Score 347.5; DB 2;
33.6%; Pred. No. 1e-20;
tive 55; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.; Barrell,
January 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.G.; Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSPDB:GN00070;
                                                                                                                                                                                                                                                                                                                                                                      Length 326;
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                                                                                                 251
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                                                                                                                                                                                                                                                                                                                                     11;
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hypothetical

protein

BH0410 [imported] -

Bacillus

halodurans

(strain C-125)

C11p11

; Bloe Fsihi

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C; Species: Bacillus
C; Date: 01-Dec-2000
C; Accession: B83701
R; Takami, H.; Nakaso
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: D83416
R; Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                                                                                                                          ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A;Reference number: A82950; MUID:20437337
A;Accession: D83416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable short-chain dehydrogenase PA1828 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
D83416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodur A; Reference number: A83650; MUID:20512582; PMID:11058132, A; Accession: B83701
A; Status: preliminary
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                                                                                                                                                                                                                                                              A;Cross-references: GB:AE004609; GB:AE004091; NID:g9947810; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-255 <STO>
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A;Residues: 1-302 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890;
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                              A;Status:
                                                                                                                                                                                                   ;Superfamily: ribitol dehydrogenase; short-chain alcohol
                                                                                                                                                                                                                           ;Gene: PA1828
                                                                                                     Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                            Genetics
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Best Local
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Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                    LDGKIAFVSGASRGIGEAIAKLLAQQGAHVIVSSRKIDGCQAVADAITAEGGKATAIACH 68
                                                           MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64
                                                                                                                                                                                                                                                                                                                                            preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHFVISESPRFVGRAVAALASDPNVSRWNGQSLSSGQLAQAYGFTDLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAFSSAETTELSGKCVVALATDPNILSLSGKVLPSCDLARRYGLRDVDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YYDLAKTSVLRMAWGLAQELQPHECTAVALTPGWMRSEIMLDHFEVTERNWRDATIKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVWQHSLDDGLRMLRLAIDTHLITSHFALPLLLKS-RGLVVEMTD-GTAEYNREHYRQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMWDDINNVGLR-----GHYFCSVYGARLMVPAGQGLIVVISSPGSLQY---MFNVP- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTGIAVPVDHLDPQKVEALVSQIERE-QGKLDVLVNDIWGG-----ELLTEWNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLIGKVALVAGATRGAGRGIAVELGAAGATVYVTGRTTRERRSEYNRPETIEETAELVTN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YGVGKAACDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM-AKEEVLQDPVLKQFK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
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                                                                                                     Conservative
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                                                                                                                          19.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erwin, A.L.; Mizoguchi, S.D.,
L.L.; Coulter, S.N.; Folger,
                                                                                                     44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
                                                                                                 Score 310; DB 2;
Pred. No. 8.3e-18
44; Mismatches 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 343.5; DB 2;
Pred. No. 1.9e-20;
7; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.D.; Warrener,
lger, K.R.; Kas,
                                                                                                                                          Length 255
                                                                                                     Indels
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                                                                                                                                                                                                                                                                              PIDN: AAG05217.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302;
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Larbig,
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Dominguez-Bernal, G.; Duchaux, ...
D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; A;Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Title: AB1077; MUID:21537279; PMID:11679669
                                  glucose 1-dehydrogenase homolog lmo1688 [imported] - Listeria monocytogen C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-20 C;Accession: AH1285 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berch ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian,
.; Dominguez-Bernal, G.; I
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
                                                                                                                                                          RESULT
AH1285
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R;Glaser, P; Frangeul, L; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AC1657
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A;Molecule type: DNA
A;Residues: 1-248 <GLA>
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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Best Local Similarity
Matches 77; Conser
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                                                                                                                                                                                                                                                                                                                                                                                          NVGDVEKVRALFKAVD-EEFGRLDVFINNAASGVL-----RPIMELEESHWDWTMNIN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLK 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHELRRHGVSCVSLWPG1VQTE----LLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIRGYYFMSIEGGKLMKEHGGGSIINVASINGVSPGEFQGI----YSVTKAAVISMTKVF 175
                                                                                                                                                                                                                                        PFGIAVNAVSGGLIETEALNHFPNREELLKDAVSK
                                                                                                                                                                                                                                                                                                                   AKALLFAGQEAAKLMQRQKSGKIISLSSIGSIRYLENYTTVGVSKAAVESLTRYLAVELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.7%; Score 286.5; DB 35.8%; Pred. No. 6.6e-16;
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    Listeria monocytogenes

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                                                      F.; Berche,
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A; Residues: 1-255 <C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                       Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology;12-194/Domain: short-chain alcohol dehydrogenase homology <SADH>
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Nature 393, 537-544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Mycobacterium tubercuiosis
C:Date: 17-Jul-1998 #Sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; nucleic acid sequence not shown; translation not shown
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69 VSQHQQVTSMLDQVTAE-LGGIDIAVCN--AGIITV----TPMLDMPLEBFQRLQNTNV
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A;Residues: 1-248 <GLA>
                                               65 SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL 124
                                                                                                                                        Status: preliminary
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                                                                                                    HGKRALITGASTGIGKRVÁLATVEAGAQVAIAARHLDALEKLÁDEIGTSGGKVVPVCCD 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Al protein Rv1928c - Mycobacterium tuberculosis (strain H37RV)
Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKALLFAGQEAAKLMORHOSGKIISLSSIGSIRYLENYTTVGVSKAAVESLTRYLAVELA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MN-KVALVTGSSRGLGREIAIALAKEGYDIAVNESRNRKKAEEVQQEIEQLGRKCVIFKA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                    nces: GB:Z84498; GB:AL123456; NID:g3261701; PIDN:CAB06498.1; PID:g1806234
source: strain H37Rv
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamlin, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                  16.7%; Score 271; DB 2;
34.6%; Pred. No. 1.3e-14;
tive 37; Mismatches 83
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                                                                                                                                                                                                                          83; Indels
                                                                                                                                                                                                                                                                               Length 255;
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Voss, H.; Wehland,
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A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, V.; A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullc Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapiduus, A.; A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Parkunthors: Schleich, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Winters, P.; Winters, P.; Winters, P.; Wingat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Togato, V.; Uch, A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subting the complete genome sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the complete sequence of the Gram-positive bacterium Bacillus subting the Gram-positive bacterium Bacillus subting the Gram-positive bacterium Bacillus subting the Gram-positive bacterium Bacillus subting the Gram-positive bacterium Bacillus subting the Gram-positive bacterium Bacillus subting the Gram-po
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;5-185/Domain: short-chain alcohol dehydrogenase homology <SADH>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucose 1-dehydrogenase homolog yfhR - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text
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                                                                                120 CAQEAAKLMEKNGGGHÍVSÍSSLGSIRYLENYTTVGVSKÄALEALTRYLAVELSÞKOIIV 179
180 NAVSGGAIDTDALKHFPNREDLLED
                                                         189 VSLWPGIVQTELLKEHMAKEEVLQD 213
                                                                                                                                             130 CSVYGARLMVPAGQGLIVVISSPGSLQYMFN-VPYGVGKAACDKLAADCAHELRRHGVSC
                                                                                                                                                                                                                                             70 EVRTLFEQVDREQOGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGHYF 129
                                                                                                                                                                                                                                                                                                                                                                                       11 VVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCVPVVCDSSQES 69
                                                                                                                                                                                                                                                                                                                                8 LVTGSSRGVGKAAAIRLAENGYNIVINYARSKKAALETÄBEIEKLGVKVLVVKANVGQPA
                                                                                                                                                                                                   KIKEMFQQID-ETFGRLDVFVNNAASGVL------RPVMELEETHWDWTMNINAKALLF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVP----YGVGKAACDKLAADCAH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.18;
33.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 262; DB 2;
; Pred. No. 6.6e-14;
40; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: A69621; PC4176; T46633
R;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, C:; Bron, S:; Brouillet, S:; Bruschi, C.V.; Caldwell, B:; Capuano, V:: Carterior

3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [validated] - Bacillus subt

A69621

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A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardnois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E., Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon, A; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Tille: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: A69501
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F;154/Active site: Tyr *status
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A;Residues: 230-246 COGU>
A;Residues: 230-246 COGU>
A;Cross-references: DDBJ:D64116; NID:g1389548; PIDN:BAA10974.1; PID:g1237012
A;Crosnan, J.E.; Morbidoni, H.R.; de Mendoza, D.
B;Cronan, J.E.; Morbidoni, 1996
J. Bacteriol. 178, 4794-4800, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: EC 1.1.1.100 [validated, MUID:96326321] A;Pathway: fatty acid biosynthesis
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A;Reference number: Z23107; MUID:96326321
A;Accession: T46633
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A;Title: The effect of Srb,
A;Reference number: JC4819;
A;Accession: PC4176
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A;Experimental source: strain 168
R;Gyquro, A.; Kakeshita, H.; Takematsu, H.; Nakamura, K.; Yamane, K.
Gene 172, 17-24, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-22,'A',24-246 <CRO>
A;Cross-references: EMBL:U59433; NID:g1502418; PIDN:AAC44307.1; PID:g1502421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 135-145 degrees
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-246 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology; Keywords: fatty acid biosynthesis; NADP; oxidoreductase; 5-185/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: fabG; srb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                   167
                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                          61
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             VVALATDPNILSLSGKVL
                                                                                                                                                                                                                NLKGVFNCTKAVTROMMKQRSGRIINVSSIVGVSGNPGQANYV-----AAKAGVIGLTK
                                                                                                                                                                                                                                                                              GLRGHYFCSVYGARLMVPAGQGLIVVISS-----PGSLQYMFNVPYGVGKAACDKLAA 175
                                                                                                                                                                                                                                                                                                                                                ADVSNPEDVQNMIKET-LSVFSTIDILVNN--AGI----TRDNLIMRMKEDEWDDVINI
                                                                                                                                                                                                                                                                                                                                                                                                              CDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNGQVCVVTGASRGIGRGIALQLCKAGATVYI--TGRHLDTLRVVAQEAQSLGGQCVPVV 62
                                                                            SSAKELASRNITVNAIAPGFISTD-MTDKLAKD--VQDEMLKQIPLA-RFGEPSDVSS--
                                                                                                                                              DCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNDKTAIVTGASRGIGRSIALDLAKSGANVVVNYSGNEAKANEVV-DEIKSMGRKAIAVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity
77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.7%;
29.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 254;
Pred. No. 2.
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83767
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04657.1; GSPDB
A;Cross-references: Strain C-125
C;Genetics:
A;Gene: BH0938.
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                      C;Species: Eubacterium sp.
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: A42468; A36439
R;Baron, S.F.; Franklund, C.V.; Hylemon, P.B.
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                                               A; Reference number: A; Accession: A42468
                                                                                                                                          A; Title: Cloning, sequencing,
                                                                                                                                                                                J. Bacteriol. 173, 4558-4569, 1991
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                     7alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) -
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Matches 76
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                                                                                          equencing, and expression of A42468; MUID:91310560
                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                    #text_change 10-Sep-1999
                                                                                                                                          gene
                                                                                                                                          coding
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J. Biol. Chem. 265, 9842-9849, 1990
A;Title: Purification and characterization of a microbial, NADP-dependent bile acid A;Reference number: A36439; MUID:90277676
A;Accession: A36439
A;Accession: A36439

A; Molecule type: protein A; Residues: 1-22 <FRA> C; Superfamily: ribitol de

ribitol dehydrogenase;

short-chain alcohol dehydrogenase homology

A; Status: preliminary

A;Cross-references: GB:M58743
A;Note: the authors translated the codon CCC for R;Franklund, C.V.; de Prada, P.; Hylemon, P.B. J. Biol. Chem. 265, 9842-9849, 1990

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A; Molecule type: DNA A; Residues: 1-266 <BAR>

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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:BA000019; PIDN:BAB73593.1; PID:g17130984; GSPDB:GN00179
A;Exper1mental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-251 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-oxoacyl-[acyl-carrier protein] reductase [imported] - Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Sim
Matches 78;
                          173 TVAKELASRGITVNAVAPGFIATD-MTSNLKSEGILQYIPLGRY------GOPEEIAG-M 224
                                                            176 DCAHELRRHGVSGVSLMPGIVOTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC 235
                                                                                                113 QAVIDLNLTGVFLCTRAVSKLMLKORSGRIINITSVAGOMGNPGQANYSAAKAGVIGFTK 172
                                                                                                                                 117 DDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAA 175
                                                                                                                                                                     67 ADVSQ------YEQVDNLINGAIDKFKRIDILVNN--AGI----TRDTLLLRMKPEDW
                                                                                                                                                                                            63 CDSSQESEVRTLFEQVDREQQG------RLDVLVNNAYAGVQTILNTRNKAFWETPASMW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 AAVVYFASDDAAYTTGQILTVSG 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 HEARHNIRCNAVLPGMTAT------DAVQDNLTDDFRNFFLKHTPIQRMGLPEEIA 223
                                                                                                                                                                                                                                                                             5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTL--RVVAQEAQSLGGQCVPVV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 ELRRHGVSCVSLWPGIVOTELLKEHMAKEEVLODPVLKQFKSAFSSAETTELSG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
VVALATOPNILSLSGKVLPSCDLARRYGLRDVDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQT----ILNTRNKAFWETPASMWDDIN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATKEETYVTMIEEI-IEQEGRIDVLVNNFGSSNPKKDLGIANTDPEVFIKTV----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKDKVILVTASTRGIGLAIAQACAKEGAKVYMGARNLERAKARADEMNAAGGNVKYVYND
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short-chain alcohol dehydrogenase homology <SADH>
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31.0%;
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                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                   Score 246; DB 2; Length 25
Pred. No. 1.3e-12;
9; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
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                                                                                                                                                                                                                                                                                                                                                          Length 251;
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Search completed: July 31, Job time: 220 sec

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A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-266 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa;Reference number: A82950; MUID:20437337.

A;Accession: F83127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: F83127
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable short-chain dehydrogenase PA4148 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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Best Local Similarity
Matches 87; Conserv
                                218 OFKSAFSSAETTELSGKCVVALATDPNI 245
                                                          171 GFSNALAKEVARDGVTVNALCPGIVGTGMWRGEDGLSGRWRQAGESEAQSWERHQASLLP 230
           231
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                                                                                                                                                                                                                                  65 SSQESEVRTLFEQVDREQOGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL
                                                                                                                                                                                                                                                                             11 LSSRVALVTGAGRGIGRGIALALARAGADVAVADLDPQVAEETAAAIRSLGRRSLALGVD 70
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Q-----GEAQTVEDMGQLVVYLACAPHV
                                                                                                       -----AHELRRHGVSCVSLWPGIVQTELLK-----
                                                                                                                                         RGVFLCCQAELPLMQAQRWGRIVNLSSI-----
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Pred. No. 2.5e-12;
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Maximum DB seq length: 2000000000
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	rala; Firmicutes; Bacillus/Clostridium group; llus/Staphylococcus group; Bacillus. TaxID=1423; PaxID=1423; PaxID=1423; PaxID=1423; PaxID=168; N=168; IN=168; In=16	RESULT 1 FABC_BACSU FABC_BACSU STANDARD; PRT; 246 AA. ID FABC_BACSU STANDARD; PRT; 246 AA. AC P51831; 031733; DT 01-0CT-1996 (Rel. 34, Created) DT 15-DEC-1998 (Rel. 37, Last sequence update) DT 16-0CT-2001 (Rel. 40, Last annotation update) DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl- BE acyl carrier protein reductase). GN FABG. GN FABG. GN FABG. OS Bacillus subtilis.

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EMBL; V43937; CAA74250.1;
EMBL; D64116; BAA10974.1;
HSSP; P50162; 1AE1.
Subtilist; B611535; fabG.
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Short-chain type dehydrogenase/reductase (EC 1.-.-).
Picea abies (Norway spruce) (Picea excelsa).
Ewkaryota; Viridiplantae; Streptophyta; Embryophyta; Ti
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                            an email to
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CAA74250.1;
BAA10974.1;
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26282 MW;
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Best Local
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HSSP; 012634; 1YBV.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                        X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

MEDLINE=98226735; PubMed=9560196;

Nakajima K., Yamashita A., Akama H., Nakatsu T.,

Hashimoto T., Odd J., Yamadda Y.;

"Crystal structures of two tropinone reductases:

stereospecificities in the same protein fold.";

proc. Natl. Acad. Sci. U.S.A. 95:4876-4881(1999).
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NP_BIND 25
ACT_SITE 179
                                                                                                                                                                              Nakajima K., Hashimoto T., Yamada Y.;
"Two tropinone reductases with different stereospecificities short-chain dehydrogenases evolved from a common ancestor.";
Proc. Natl. Acad. Sci. U.S.A. 90:9591-9595(1993).
         Yamashita A., Kato H., Wakatsuki S., Tomizaki T.,
Nakajima K., Hashimoto T., Yamada Y., Oda J.;
                                     X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-99316165; Pubmed-10387002;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    Datura stramonium (Jimsonweed) (Common thornapple).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Datura.
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16-0CT-2001
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96 (Rel. 34, Last sequence update)
01 (Rel. 40, Last annotation update)
reductase-II (EC 1.1.1.236) (TR-II).
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tropinone reductase-II complexed
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Pred. No. 8
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RESULT 4
Y4LA_RHISN
ID Y4LA_RHISN
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DT 01-NOV-1997
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Bacteria; Proteobacteria;
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01-NOV-1997
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01-NOV-1997
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Ox1doreductase; NADP; 3D-structure.
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PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
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PROSITE; PS00061; ADH_SHORT; 1.

Hypothetical protein; Oxidoreductase; Plasmid.

NP_BIND 10 34 NAD OR NADP (BY SACT_SITE 159 159 BY SIMILARITY.

SEQUENCE 278 AA; 28743 MW; 1DD105675555000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _AQUAE
  Nature
                                                            MEDLINE-98196666; PubMed-9537320; Deckert G., Warren P.V., Gaasterland T., Young Graham D.E., Overbeek R., Snead M.A., Keller N Feldman R.A., Short J.M., Olson G.J., Swanson "The complete genome of the hyperthermophilic
                                                                                                                                                                                                                                                                                                          FABG OR AO_1716.
                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DCC-1998 (Rel. 40, Last annotation update)
3-oxoacy1-[acy1-carrier protein] reductase (Eacyl carrier protein reductase).
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                                                                                                                                                                                                                                         Bacteria; Aquificales;
NCBI_TaxID=63363;
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                                                                R.V.;
bacterium
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                                                                                                            A.L.,
Huber
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                   GNO_GLUOX
P50199;
01-OCT-1996
         Klasen R., Bringer-Meyer S., Sahm H.;

*Blochemical characterization and sequence analysis of the gluconate:NADP 5-oxidoreductase gene from Gluconobacter ox J. Bacteriol. 177:2637-2643(1995).

-I. FUNCTION: INVOLVED IN THE NONPHOSPHORYLATIVE, KETOGENI OF GLUCOSE AND OXIDIZES GLUCONATE TO 5-KETOGLUCONATE. NADP, ALMOST INACTIVE WITH NAD.
                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Ace Gluconobacter.
                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gluconate 5-dehydrogenase (EC 1.1.1.69) (5-keto-D-gluconate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP_BIND
ACT_SITE
SEQUENCE
                                                                                                    STRAIN=DSM 3503;
MEDLINE=95270578; PubMed=7751271;
                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                          G
NO
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                                                                                                                                                      NCBI_TaxID=442;
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PATHWAY: FIRST I
PATHWAY:
SIMILARITY: BELA
     CATALYTIC
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                                                                                                                                                                                                                                                                                                                                                    KELAPRNVLVNAVAPGFIETDM-----TAVLSEEIKQKYKEQIPLGRFGSPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDI 119
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ND 12 36 NADP (BY SIMILARIY
ITE 157 157 BY SIMILARIY
NCE 248 AA; 26867 MW; 5CFD9EB9AD83F2C;
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E; PS00061; ADH_SHORT
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                                                                                                                             SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%;
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D-gluconate + NAD(P)(+) = 5-dehydro-D
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Pred.
                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                          256 AA
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                                                                                                                          CHARACTERIZATION
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                                    KETOGENIC OXIDATION
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Best Local s
Matches 66
           SEQUENCE FROM N.A.

STRAIN-MSD8 / DSM 3109;

MEDLINE-9289316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.S.,

McDonald L., Utterback T.R., Malek J.A., Filhilps C.A., Richardson D.

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Byidence for lateral gene transfer between Archaea and Bacteria fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                      Thermotoga maritima.
Bacteria; Thermotogales;
                                                                                                                                                                                                                      FABG OR TM1724
                                                                                                                                                                                                                                                                                                     FABG_THEMA
Q9X248;
                                                                                                                                                                            NCBI_TaxID=2336;
                                                                                                                                                                                                                              30 MAY-2000 (Rel. 39, Created)
30 MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
3-oxoacyl-[acyl-carrier protein] reductase
acyl carrier protein reductase).
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NP_BIND 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X80019; CAA56322.1; -. HSSP; P47227; 1BDB.
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SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                 STANDARD;
          of Thermotoga maritima.";
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O THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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Pred. No. 2.8e
32; Mismatches
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P73574;
P73574;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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SEQUENCE
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakai Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura 'Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yabata S.;
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FABG1 OR SLR0886.
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HSSP; P50162; 1AE1.
TIGR; TM1724; -.
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                                                                                                                 SEQUENCE FROM N.A. MEDLINE-97061201; Pu Kaneko T., Sato S.,
                                                                                                                                                                                                                                                                     Synechocystis sp. (strain Bacteria; (yanobacteria; )
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PF00106; adh_short; 1.
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10 34 NADP (BY SI)
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246 AA;
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Epermatophyta; Magnoliophyta;
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TISSUE-Cultured
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No. 1.1e-10
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PRINTS; PR00081; GDHRDH.
PROSITE; PS00061; ADH_SHORT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakajima K., Hashimoto T.;
"Tropinone reductase-II gene of Hyoscyamus niger.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CATALYZES THE STEREOSPECIFIC REDUCTION OF
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Nakajima K., Hashimoto T., Yamada Y.;
"CDNA encoding tropinone reductase-II
Plant Physiol. 103:1465-1466(1993)
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            nl-carrier protein] reductase, chloroplast precursor (3-ketoacyl-acyl carrier protein reductase)
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; 28437 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 214; DB 1;
Pred. No. 1.4e-10;
9; Mismatches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADP (BY SIMILARITY).
BY SIMILARITY.
; 6CA7AF85CAA128FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hyoscyamus niger.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118;
                                                                                                                                                                                                                                           -NLDKLIDRCALRRMGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TROPINONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                      243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta-ketoacyl-ACP reductase.";

MOI. Gen. (233:122-128(1992).
-i- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-(acyl-carrier protein)
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
-i- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                        PRINTS; PR00080; SDRFAMILY
                                                                                                                                                                                                                 HSSP; P50162; 1AE1.
InterPro; IPR002198; ADH_short.
                                                                                                                                                                                                                                                   EMBL; X64566; CAA45866.1; -. PIR; S19832; S19832.
                                                                                                                                                                                                         Pfam; PF00106; adh_short
                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>-</del>
                                                                                                                                                           Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein B., Pawlowski
Toepfer R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-92293104; PubMed-1376402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Myrtales; Lythraceae; Cuphea.
NCBI_TaxID=3930;
                                                                                                                                             ransit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMOTETRAMER SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                (SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PLASTIDS
                                                                                                                                                                            PS00061;
                                                       82
227
320
                                                                                                                    62
                                                        AA;
                                                                                                                                                                         ADH_SHORT; 1.
                                                       106
227
33103
                                                                                                                61
320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoericke-Grandpierre C.,
                                                        MW;
                                                                                                                                                      Oxidoreductase; NADP; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROBABLE).
CHLOROPLAST AND NON-PHOTOSYNTHETIC
                                                                     ВΥ
                                                                                    NADP
                                                                                                             CHLOROPLAST (BY SIMILARITY)
3-OXOACYL-[ACYL-CARRIER PRO
                                                    06BAF0522B2BBC87 CRC64
                                                                      SIMILARITY
                                                                                 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Embryophyta; Tracheophyta;
edons; core eudicots; Rosid
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                                                                                                             PROTEIN
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Matches
       275
                                 247
                                                           251
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                                                                                                                  191
                                                                                                                                                                        139
                                                                                                                                              128
                                                                                                                                                                                                  89
                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                               9 VCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCVPVVCDSSQ
               SLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG
                                                                                                        FLCTQAAAKIMMKKKKGRIINIASVVGLVGNAGQANYSAAKAGVIGFTKTVAREYASRNI
                                                          NVNAVAPGFISSDMTSK---
                                                                             SCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALATDPNIL
                                                                                                                                 YFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCAHELRRHGV
                                                                                                                                                                                 ESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMMDDINNVGLRGH
                                                                                                                                                                                                                    VVIVTGASRGIGKAIALSLGKAGCKVLVNYARSSKEAEEVSKEIEAFGGQALTFGGDVSK
                                                                                                                                                                    EEDVEAMIKTA-VDAWGTVDILVNN--AGI----
                                                                                                                                                                                                                                                                                               Similarity
KILETIPLGRYGQPEEVAG--LVEFLAINPASSYVTG
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                            13.28;
                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                            Score 214; DB 1;
Pred. No. 1.8e-10;
1; Mismatches 108
                                                                                                                                                               -TRDGLLMRMKKSQWQEVIDLNLTGV
                                                                                                                                                                                                                                                                               108;
                          287
                                                                                                                                                                                                                                                                                                        Length 320
                                                                                                                                                                                                                                                                              Indels
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                                                                                                          250
                                                                                                                                     186
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Best Local S
Matches 65
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YCP1_BRAJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Probable short-chain type dehydrogenase/reductase (EC 1.--.).
Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID-375;
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                          NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bradyrhizobium japonicum that is expressed anaerohically.";

Appl particulary and a cytochrome P-450 locus from symbiotically.";
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U12678; AAC28892.1; -. HSSP; P08074; 1CYD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 1398:243-255(1998).
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification and sequencing of a cytochrome P450 gene cluster Bradyrhizobium japonicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-USDA 110;
Tully R.E., Keister D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q45219;
01-NOV-1997
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98322110; PubMed-9655913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Appl. Environ. Microbiol. 59:4136-4142(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
180
                           184
                                                       120
                                                                                  125
                                                                                                                                                                                                                                                                                                                                    ypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                               interPro;
                                                                                                            64
                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SDR) FAMILY
                        HGVSCVSLWPGIVQTELLK - - EHMAKEEVL
                                                                                                                                                              GKVAVVTGAGAGIGKACALAIAREGGRVVVA--DIDGSAAIACTAQIAAEAGHALALAID
AQIRCNAVAPGLIMTERLRMQTHLRRHQLL
                                                    RGTLLCCRQAIPRMIARGGGAIVNMSSCQGLSGDTALTSYAASKAAMNMLSSSLATQYGH 179
                                                                               RGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCAHELRR 183
                                                                                                         IADAQAVAALFETAER-HFGGVDLLVNNASA---MHLTPRDRAILELELAVWDQTMARNL
                                                                                                                                     SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL
                                                                                                                                                                                           GQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQ--SLGGQCVPVVCD
                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                            IPR002198; ADH_short.
                                                                                                                                                                                                                                                                                            10
159
275 AA;
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                          159
                                                                                                                                                                                                                                      13.2%;
                                                                                                                                                                                                                                                                                              28827 MW;
                                                                                                                                                                                                                                                                                                                                      Oxidoreductase.
                                                                                                                                                                                                                       34;
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; 312E7070C404DF86 CRC64;
                                                                                                                                                                                                                                      Score 213.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                         Mismatches
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A
                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                Length 275;
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                                                                                                                                                                                                                      Gaps
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Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
MCDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y019_THEMA
Q56318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X85171; CAA59459.1; -. EMBL; AE001690; AAD35113.1; HSSP; P19992; 1HDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular and phylogenetic characterization of pyruvate and 2-
keto1sovalerate ferredoxin oxidoreductases from Pyrococcus furiosu.
and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.";
J. Bacteriol. 178:248-257(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermotoga maritima. Bacteria; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome sequence of Thermotoga maritima.", Nature 399:323-329(1999).
-1- SIMILARITY: BELONGS TO THE SHORT-CHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
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MEDLINE-96125254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TM0019
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00106; adh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kletzin A., Adams M.;
                                                                                            60
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                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SDR) FAMILY.
                                         GLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNV-PYGVGKAACDKLAADCAHEL
NLTGPYICSRYCAEEMIKRGGGVIINIASTRAFQSEPDTEPYSASKGGLVALTHSLAVSL
                                                                                                                    LEGKVAVVTGGGQGIGAAIAQLFAENGMKVVIA--EIDEEAGVEREEMLRERGLDVTFVK
                                                                                                                                                                                                                               MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQE--AQSLGGQCVPVV
                                                                                       TDVADENSVKNMVRKT-VEIYGGVDVLVNN--AAVMSV----KSIFERPLEEWERVIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TM0019;
                                                                                                                                                                                                                                                                                75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO0080; SDRFAMILY.

PRO0081; ADH_SHORT; 1.

;; PS00061; ADH_SHORT; 1.

NADP; Complete

NADP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                             153
130
256 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35, Created)39, Last sequence update)40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3109;
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                                                                                                                                                                                                                                                                                                                                                                                                                      33
153
136
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                                                                                                                                                                                                                                                                                                   12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TM0019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *Molecular cloning of higher-plant 3-oxoacyl-(acyl-carrier protein) reductase. Sequence identities with the nodG-gene product of the nitrogen-fixing soil bacterium Rhizobium meliloti.";
Biochem. J. 283:321-326(1992).
-!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) - 3-oxoacyl-[acyl-carrier protein] + NADP(+) - 3-oxoacyl-(acyl-carrier protein] + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+) - 3-oxoacyl-(acyl-carrier protein) + NADP(+
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Slabas A.R., Chase D., Nishida I., Murata N., Sidebottom
Safford R., Sheldon P.S., Kekwick R.G.O., Hardie D.G.,
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01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacy1-(acy1-carrier protein) reductase, chloroplast precursor
(EC 1.1.1100) (3-ketoacy1-acy1 carrier protein reductase).
Arabidopsis thaliana (Mouse-ear cress)
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3-OXOACYL-[ACYL-CARRIER PROTEIN]
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PROSITE; PS00061; ADH_SHORT; 1.
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                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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DNA Res. 2:61-69(1995).
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16-OCT-2001
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Yoshida K.-I., Seki S., Fujimura
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262 AA;
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation updat
oxidoreductase yxbG (EC 1.---
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                                                                                                                                                                       Yamamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia corresponding to the 28.0-40.1 min region DNA Res. 3:363-377(1996).
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P25529;
STRALM-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpattick H.A.

Posfai G., Hackett J., Klink S., Boutin A., Shao Y.; Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K
                                                                                                                                                                                                                                                               Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M. Kitagawa M., Makino K., MIKI T., Mizobuchi K., Mori H. Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nis Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C Yamamoto Y., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli, and Escherichia coli 0157:H7.
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                                                                                                                          SEQUENCE FROM 1
STRAIN-0157:H7
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Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono
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Mau B., Sh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
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                                                                                                                                                 N.A.
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Rode C.K., Mayhew G.F.
Goeden M.A., Rose D.J.,
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on the linkage
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H.A.,
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MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., T
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EcoGene; EG10425; hdhA.
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Welch R.A.,
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CATALYTIC ACTIVITY: 3-alpha,12-alpha,12-alpha-trihydroxy-5-beta-cholanate + NAD(+) = 3-alpha,12-alpha-dihydroxy-7-oxo-5-beta-cholanate + NADH.

SUBUNIT: HOMOTETRAMER.
SUBUNIT: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASE
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JT0951; JT0951
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D90805; BAA15370.1;
D90806; BAA15377.1;
D90808; BAA15407.1;
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용	69	69 ITSEQELSALAD-FAISKLGKVDILVNNAGGGGPKPFDMPMADF 111	
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용	112	112 RRAYELNVFSFFHLSQLVAPEMEKNGGGVILTITSNAAENKNINMTSYASSKAAASHLVR 171	
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FOR SEQ HARACTEI 313 am. nino ac. NESS: 1 11nea SOURCE: PROSNO 356351	APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PF-0475 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555 TELEPHONE: 650-845-4166	STATE: CA COUNTRY: USA ZIP: 94304 ZIP: 94304 CMPUTER READABLE MEDIUM TYPE: D1 COMPUTER: IBM C OPERATING SYSTEM SOFTWARE: FastS URRENT APPLICATION NUMB FILING DATE: F1 CLASSIFICATION:	RESULT 1 US-09-019-216-1 Sequence 1, Application US/09019216 Patent No. 5928923 GENERAL INFORMATION: APPLICANT: LAL, Preet1 APPLICANT: Corley, Neil C. TITLE OF INVENTION: HUMAN SHORT CHAIN DEHYDROGENASE NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto	7 7 2.2 464 2 US-08-834-108-68 7 2.2 525 4 US-08-542-634-2 9 7 2.2 525 5 PCT-US95-13703-2 9 7 2.2 532 4 US-09-008-271A-3 1 US-08-542-634-2 9 7 2.2 540 4 US-08-542-634-2 9 7 2.2 549 4 US-08-542-634-2 9 7 2.2 549 4 US-08-477-292-1 549 4 US-08-4	27; 4 US-08-477-292- 27; 5 PCT-US95-13703 27; 5 US-09-043-627- 16 1 US-08-252-995D 16 2 US-08-834-108- 36 1 US-08-259-148A 36 1 US-08-259-148A 36 2 US-07-876-941A
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                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                                                                                                                                                         NAME: B111ings, Lucy J. REGISTRATION NUMBER: 36,749 REGISTRATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                  IMMEDIATE SOURCE:
                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN SHORT CHAIN DEHYDROGENASE
NUMBER OF SEQUENCES: 3
MEDIA.
LIBRARY: Gen.
- ONF: 2315796
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CITY: Palo Alto
                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                           TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                   LING DATE:
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                                                                                                                                                                                                                                                                                                                                                                               WARE: FastSEQ for Windows Version 2.0 PAPPLICATION DATA: ICATION NUMBER: US/09/019,216
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                                                                                                             323 amino acids
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                                GenBank
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                                                     Query Match
Best Local S
Matches 10
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Best Local S
Matches 16
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,962B
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 6-October-1 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                          FEATURE:
                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                           NAME/KEY:
10
             12 VTGASRGIGR 21
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                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
VTGASRGIGR 19
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5, 5731195
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                                                       l Similarity
10; Conserv
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16; Conser
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                                                                                                                                                                                                                                            244 amino acids
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHRISTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT
                                                                                                                                          E.coli 3-oxoacyl(acyl carrier protein)
reductase (FABG)
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                                                                                                                                                                                     protein
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                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                          838-3884
                                                                                                                                                                                                                                                                                                                                                                Patricia A.
                                                                 3.2%; Score 10;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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Pred. No.
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                                                                DB 1;
0.079;
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                                                                              Length 244;
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US-08-562-114B-13 ; Sequence 13, Application US/08562114B

RESULT

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Best Local
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                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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FILING DATE: 20-January-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kohli, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 805 Third Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                          10 VTGASRGIGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase NAME/KEY:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/562,114B FILING DATE: 22-No. 5972646ember-1995
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                                                                                                                      ADDRESSEE
                                                                                                                                   RRESPONDENCE ADDRESS:
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TLE OF INVENTION:
TLE OF INVENTION:
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                                                                            SEE: Felfe & Lynch
1: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i: 244 amino acids amino acid
                                                                                                                                                                                                                                                                                                  Application US/08729594A
                                                                 New York
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Wordperfect 5.1 and ASCII
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NO: 13:
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                                                                                                                                                                                     Ulf; Simon, Andras; Romert, Anna
ISOLATED NUCLEIC ACID MOLECULE WHICH
CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASI
ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOLATED NUCLEIC ACID MOLECULE WHICH CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL HYROGENASE ACTIVITY, AND WHICH ASSOCIATES WITH P63, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                        RETINOL BINDING PROTEIN
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Vers
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-238-481-2
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                                                          Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conser
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                                                                                                                                                                                                                                                                                                APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: FabG
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/238,481
CURRENT FILING DATE: 1999-01-28
                                                                                                                                                                                                                                                                                      FILE REFERENCE: GM10192
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FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: Wordper
                12 VTGASRGIGR 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VTGASRGIGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
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9 VTGASRGIGR
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Best Local
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CURRENT FILING
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SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
                                                                                                                                                                                                                                                         PPLICANT: Baltz, Richard H
PPLICANT: Broughton, Mary C
PPLICANT: Crawford, Kathryn P
PPLICANT: Crawford, Kishnamurthy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-036-987A-21
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                     f: Waldron, Clive
INVENTION: Biosynthetic Genes For Spinosyn Insecticide
ERENCE: 50489 DIV1
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Broughton, Mary C.
Crawford, Kathryn P.
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 255
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Best Local Similarity

Matches 10; Conserv
                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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TYPE: PRT
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                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 713.787.1400
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                      NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:132
   STRANDEDNESS
                                                                                                                                                                              APPLICATION NUMBER: GB90/
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/793,035
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              amino acid
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                              amino acids
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single
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Pred. No.
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Query Match
Best Local Similarity

3.2%;

Score 10; Pred. No.

Matches

Mismatches

APPLICANT:

Bringer-Meyer, Stephanie

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                                                    RESULT 11
US-08-594-808B-7
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US-08-793-035-10
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US-08-793-035-10
                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
                         quence 7, Application US/08594808B tent No. 5804423
                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: 713.787.1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
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  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION:
                                                                                                           76
                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                             NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 77210-4433
                                                                                                                                  11 VVTGASRGIG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0
FILING DATE: 28-JUL-1997
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                                                                                                        VVTGASRGIG 85
              INFORMATION:
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                                                                                                                                                                                                                                                                               315 amino acids
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Klasen, Ralf
                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08762129 Patent No: 5756299
                                                                                                                                                                                                                     APPLICANT: Hillman, Jenux.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 1989
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
      SOFTWARE: FASTER: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,129
FILING DATE: Herewith
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1:0, Version #1:30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/594,808B FILING DATE: 07-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: M.
                                                                                                                                     COUNTRY:
ZIP: 943
                                                                                                                                                                                                                                                                                                                                                                                                                        16 VTGASRGIG 24
                                                                         COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CLASSIFICATION:
                                                                                                                                                                                      CITY:
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ZIP: 10471-0900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: The Firm of Karl F. Ross, 5676 Riverdale Ave.
                                                                                                                                                                                                3174 Porter Drive
                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            718/601-1099
                                                                                                                                                                                                                                                                                             Hillman, Jennifer L.
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                                                                                      IBM Compatible
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                                                                                                          Diskette
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RIOR APPLICATION DATA:

PPLICATION NUMBER:

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                                                                               REFERENCE/DOCKET NUMBER: FEI
ELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                   STRANDEDNESS
                                                                                                                     NAME: Mueller, Lisa L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         COUNTRY:
                                          ENGTH:
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180 N. Stetson, Suite
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US-08-858-207A-270
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US-08-858-207A-270
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Best Local Similarity
                                                                            MOLECULE TYPE:
                                                                                                                       SEQUENCE CHARACTERISTICS
LENGTH: 186 amino acid
                                                                                                                                                                              TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     SOFTWARE: FASTSED FOR WINDOWS VERSION 2.0 CURRENT APPLICATION DATA, APPLICATION NUMBER: US/08/858,207A FILING DATE: 09-MAY-1997
                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE
                                                                                         COPOLOGY:
                                                                                                                                                                       ELEFAX:
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                   NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       CIFIC King of Prussia STATE: PA
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       Similarity 7; Conserv
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6348328
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                                                                                                                     186 amino acids
    Conservative
                                                                                                                                                                    610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hodgson, John
Knowles, David
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  ed. No. 47
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Mismatches
             DB 4;
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                     Length 186;
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Query Match

score 8;

Length 277;

-08-762-129-5

MMEDIATE SOURCE:

linear single

IBRARY:

118519

GenBank

STRANDEDNESS:

amino acid

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 277 amino acids

5:

ELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555

PF-0171 US

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF

/AGENT INFORMATION:

TELEFAX:

415-845-4166

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US-09-239-052-2
Sequence 2, Application US/09239052
Fatent No. 6346395
CENERAL INFORMATION:
APPLICANT: Homes, David J.
APPLICANT: Debouck, Christine
APPLICANT: Debouck, Christine
APPLICANT: Debouck, Christine
APPLICANT: Mang, Min
APPLICANT: Mang, Min
APPLICANT: Momarka, Anna L.
APPLICANT: Momarka, Anna L.
APPLICANT: Chalker, Alison F.
APPLICANT: Chalker, Alison F.
APPLICANT: Chalker, Alison F.
APPLICANT: So, Chi Young
APPLICANT: So, Chi Young
APPLICANT: So, Chi Young
APPLICANT: Mallis, Nicola G.
APPLICANT: Ballis, Nicola G.
APPLICANT: Wallis, Nicola G.
APPLICANT: Parson, Stewart C.
TITLE OF INVENTION: FabG
FILE REFERENCE: GM10191
CURRENT APPLICATION NUMBER: US/09/239.052
UNMAER OF ESO ID NOS: 2
INVERSE OF ESO ID NOS: 2
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